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E12754 Gentianatri
AB026494 Gentiana
E12756 Perilla oci
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Copyright (c) 1993 - 2000 Compugen Ltd.
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421 CACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAA 480
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                                                          precursor'
                                                                                                                                                                  Length 1703;
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    1703
    organism='Gentianatriflora'

    1415
    product='acyltransferase

                                                                           /product='acyltransferase'
Location/Qualifiers
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0
                 /variety='japonica'
/tissue_type='petal'
/clone='pGAT4'
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                                                                                                        /organism="unidentified"
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Matches 1703; Conservative
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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AP000200 Homo sapi
  AC002560 Genomic
AX025514 Sequence
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691!
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1703)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 1 18-MAR-1997;
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CNS01DXJ
CNS01DW6
CNS01DX6
AC016299
AR105363
         AX025514
AP000606
AC074226
AB016892
AC069470
                                                       AB028618
AC069470
AC087724
AB028618
AX083744
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AL356295
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strandedness: Double;
topology: Linear;
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AB010708 1679 bp mRNA PLN 20-FEB-1999 Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,

AB010708.1 GI:4185598 Anthocyanin 5-aromatic acyltransferase.

complete cds. AB010708

DEFINITION RESULT AB010708 LOCUS

ACCESSION VERSION KEYWORDS

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             CACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,C12R1:865).
CC (C12N9/10,C12R1:19);
CC strandedness: Double;
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                    ACCACACGAGGTTCAATCACTAGAAGGTTGTACTTCATAAATTCCAGAGGTCGAATATA
                                                                                        TGAAGGTTCTTGAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCGAGTTAT
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukui, Y.,
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Senecio cruentus mRNA for acyltransferase,,partial cds
E12757
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M.,
Yonekura,K., Mizutani,M. and Kusumi,T. .
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER
PATENT: JP 1997070290-A 5 18-MAR-1997;
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/tissue_type*'petal'
/clone*'pCAT48'
1.1367
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/organism="unidentified"
/db_xref="taxon:32644"
1 293 c 296 g 477
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17-FEB-1995 JP 95P 671
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JP 1997070290-A/5
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unclassified
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                                                                                                  AACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGTTGTT
                                           647 AAATAAGTTGAGACATACAAG----GCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTG
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CGTTATCTCTTACTTCGTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTT
                             TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTA
                                                                                   AGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGC
                                                                                                                                          CGATCAA-----ATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCG
                                                                                                                                                                       238 TTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTG
                                                                                                                                                                                                   ACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATC
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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AGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCT 1275
                                                                           1336 AGATIGGAGIAICATIGCCIMAGAITCATAIGGAIGCAITIGCAAAAAICITIGAAGAAG 1395
                                                                                                                                     57 TCAAAGTTCTTGAGAAATGCCGTCTTGCCCACCACCGGAC---GCCGTCGCCGGGTTA 113
                                                                                                                                                                                                                                                                                        E12754 1622 bp DNA PAT 24-JUN-1998 Gentianatriflora mRNA for acyltransferase, complete cds. E12754 E12754 JP 1997070290-A/2. unidentifled.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASSHIRARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
              CTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1623)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 2 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
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    .1622
/organism='Gentiana triflora'

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Pred. No. 1e-37;
0; Mismatches 618; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type='petal'
/clone='pGAT106'
35. .1474
/product='acyltransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
345 c 322 g 47
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strandedness: Double;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gentianatriflora
JP 1997070290-A/2
18-MAR-1997
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52.2%;
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Best Local Similarity 52.28
Matches 728; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       unidentified
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SYGLTIAESSNFDLIDGLDGRDSYRFNDLIPDLPEPTYSOBPULPFALVYFKSD
TGYSTIAESSNFDLIDGLRDSYRFNDLIDGLPEPTYSOBPULPFALVYFSN
TGICIGRNLHQOVLGDASSFLHFNKLWYLDKSNGSNGSLKFLFLSSLBWYDRSVYODPFH
IRRIYNBRKLLKSQGTPTVLNPAISKDEVRATFILHPIDIMKLKKFISKRNRNLTGS
SYNLSFFFYTYSALLWFCLSKSLDTVVREKVEEBKHAANLCAFINCRGFAPFPPQNY
FGNCIVPCWYGSTHEDVURGELSVAAFAIGDAIHKRLHDYGSILGEDWISFPRSTSA
APRSTLIYVVGSAQRNVHDFDADFGWCKLEKHESVSTNPSATLLISKSRRFKGALEL
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                                              GGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTG 1257

TTGGATCCGCACAACCCAATGCATTTTGATGATTTTGGATTGGGGAAAAGCTTG 1298
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Yujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular clonding and blochemical characteization of
hydroxycinnmamoyl-Coh:anthocyanin
3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana
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( pases I to 162)

Tandka,Y. and Yonekura-Sakakibara,K.

Direct Submisted (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental R Wakayama-dai I-1. Shimamoto, Osaka 618-8503, Japan (E-mail:Yoshikazu_Tanaka&Suntory.co.jp, Tel:81-75-962-8807,
                                                                                                                                               CAAAATTTGACA - - - TTACCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCA
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/protein_id="BAA93452.1"
/db_xref="GI:7415597"
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/db_xref="taxon:55190"
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Gentiana triflora
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FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
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     GGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATGCAT 1374
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Perilla ocimoides mRNA for acyltransferase,partial cds.
E12756
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
PI FUKUI YUKO. VANDENTI.
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070:390-A 4 18-MAR-1997;
SUNTORY LTD
OS PETILIA COLL
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/organism='Perilla
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/organism="unidentified"
/db_xref="taxon:32644"
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strandedness: Double;
topology: Linear;
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JP 1997070290.A/4
18-MAR-1997
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                                                                     CCCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTC 144
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      Length 1622;
                               Indels
Pred. No. 1e-37; Mismat.
                             0; Mismatches 618;
     11.1%; Score 189.2; 52.2%; Pred. No. 1e-
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                     Gaps
                                                                                              AATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTG
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                                                                                  TCCCTTCTGTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCT
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                     48;
 Length 1479;
                   0; Mismatches 668; Indels
DB 10;
          Pred. No. 2.2e-33;
 Score 172.2;
 10.1%;
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                     701; Conservative
          Similarity
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/translation="v155646"
/translation="tvefcrwcpppbbsvaeosypLrFFDMTWLHFHPWLQLLFYEFPC
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HHTVSDAPSFLAFITHAMSSWSHTENDEDEDEEFKSLPVFDRSVIKYPFKFDSIYWRNA
LKFPLOSRHPSLPTRTFVFTGSKIKKLKGWIOSRVPSIVHLSSFVAIAAYWWAG
ITKSFTADBEDQDNEDAFFLIPPULRPRENDPYPTGOLGSYALPRWRRELVGEKG
VFLAAEVIAALBIKKRINDKRILETVEKWSPBTRKALQKSYFSVAGSKG
VFLAAEVIAALBIKKRINDKRILETVEKWSPBTRKALQKSYFSVAGSKG
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VFLAAEVIAALBIKKRINDKRILETVEKWSPBTRKALQKSYFSVAGSKG
VFLAAEVIAALBIKKRINDKRILETVEKWSPBTRKALQKSYFSVAGSKLDIVGADFGW
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Perilla frutescens mRNA for anthocyanin acyltransferase, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTTGATTATGCAGAATTG - - - ATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGT
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2 (Dases I to 1476)
Sakakibara, K.Y. and Tanaka, Y.
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Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla
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    1476
    /organism="Perilla frutescens"
    /db_xref="taxon:48386"

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Perilla frutescens leaf cDNA to
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Burasicales; Brassicaceae; Arabidopsis.

1 (bases i to 119914)
1 (bases i to 119914)
1 (bases i to 119914)
1 Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Walker, M., Yu, G., Schwartz, J., Shinn, P., Toriumi, M., Vysotskala, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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AGAATGCGGCGGGGAGAGCT3GTGGGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATC 1028
                                                                                                                                                                                                                                                                                                                                                                                                              Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Hulzar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremenetskala, I., Kin, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Walker, M., Yu, G., Bcker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                               GCGGCGGAGATAAAAAAAAGGAT - - - CAACGACAAGAGAATATTAGAAACGGTGGAGAAA
                                                                                                                                              TGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCT
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                                                               GGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACT
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Stanford University, 855 California Avenue, Palo Alto,
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                                                                                Length 1476
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Pred. No. 3.6e-33;
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Center, CA 94304,

COMMENT

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GESEDSEMPROVSRRSGGTDSSRRGSPLPTSEESDPRPRHOWTERQLSDHLLLYER
GESEDSEMPROVSRRSGGTDSSRRGSPLPTSEESDPRPRHOWTERQLSDHLLLYER
FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNRKTQDP
TLLEMBESLRSDDPDYVKAQNHQWYYESFWYISFVLCLENSNLRCVVIFCVQQLPK
SHPEQDSKRKRDITASDAMBHLKVPKRENNLMQKSADIDCNGKCSANSDDQLSEKIS
KALEQTSSNITICGFCQSARVSEATGEMLHYSRGRPVDGDDIFRSNVIHVHSACIEWA
POYYYEGDTWNLKARELARGMKIKCTRCSLKGAALGGFWKSCRRSYHVCAREISRCR
WDYEDFLLCPAHSSVKFPNRKSGRRVNRAAPLPKINPAELCSLEQTPAFTKELVLCG
SALGKSDKKLMSLANFRYTSRYMNPSVTHYIASPDEKGACTRTLKYLMGILMGKW
INAAWMKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRAETNKPKLFEGLKFYFF
GDFYKGYKBDLQNLVKVAGGTILNTEDBELGAESSNNNNDQRSSSIVVYNIDPPHGCAL
GEEVYIINQRANDBAALASQTGSRLVGHTWULESIAGYKLHPVIG"

//gone=#F21M11 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jóln(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
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LHFGSMCCSKSKCDGMDAMIPDIDDTLLSTIPPHKRNGFFGGERLNSTRFEDWIQKKR
APAVPHHKKLYHDIFREKGIKIFLISSRKEYLERSATVDNLIQAGYYGNRULMLRGLEDQ
QKEVKQYKSEKRKWLMSLGYRVWGVMGDQWSSFAGCPLPRRTFKLNSIYYVA"
complement(join(14004. 14312, 14565. 14641, 14787. 15831,
15906. 16006, 16137. 16362))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTKLEERDLYFHKLKLFFFTALKLRGGPSIVFAHSMGNNVFRYFLEWLRLEIAPKHYL
KWLDQHIHAYFAVGAPLLGSYBAIRSTLSGYFFGLPVSEGTARLLSNSFASSLWIMPF
SKNCKGDNTFWTHFSGGAARKDRRVYHODEERYQSYSGWPTNINIEIPSTSARELA
DGTLERAIEDYDDPSKRMLAQLKKYVPFFVIRNIAHRSSLAGFLLYHDDPVFNPLTPW
ERPPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDNWIITDIIYETEGSLVSRSGTVVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKGRTKQKQSQKENSNFIADQEEKRDSSFGTDPQIDDITLSVKPKCRIEPKKLRNQE
LAVDASLSYWLSTSESGEONSASWTLTPEKLKSTGCYSKPLRINHDDRPVLCALTL
EDIKQFSATSTPRKSPEKSPDETPIIGTVGCYWGNRSKAIDCGSASSFKGIPNTSSKY
REDKGYWHGTPFERALEKAINNIDK"
COMPLEMENT (16835. . . 20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MLDQISGNHTHEKLSVETAEPHHLNDRVHIVEEIPKASVIPITE
ICDEAEEKCSPSTISRKRVTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDBEFYSDVGFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGANSKSVTASFTVIAVFFLICGGRTAVEDETEFHGDYSKLSGI
IIDGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKWCVEFGIEANAIVAVPYDWRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(16835. 17185,17274. 17392,17491. 17656,
17795. 17885,17982. 18079,18175. 18361,18504. 18604,
18705. 19049,19134. 19349,19439. 19791,19862. 19967,
20188. 20238))
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\[ \frac{1}{2} \text{xrd} = \frac{1}{4} \text{204.288} \]

\[ \frac{1}{4} \text{xrd} = \frac{1}{4} \text{204.88} \]

\[ \frac{1}{4} \text{xrd} = \frac{1}{4} \text{204.88} \]

\[ \frac{1}{4} \text{xrd} = \frac{1}{4} \text{204.88} \]

\[ \frac{1}{4} \text{xrd} = \frac{1}{4} \text{xrd} \text{xrd} \text{xrd} \]

\[ \frac{1}{4} \text{xrd} = \frac{1}{4} \text{xrd} \text{xrd
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HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(14567. .14641,14787. .15831,15906. .16006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16327. .16362))
/gene="F21M11.3"
/note="Unknown protein; Location of ESTs 40C3TT,
gp|AA728590 and40C3T7, gb|T04573"
/codon_start=1
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                               complement(14004. .16362)
/gene="F21M11.3"
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/db_xref="GI:4204287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD10667.1"
/db_xref="G1:4204286"
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/gene="F21M11.6"
27777. .28734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AC002560)

e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
Genes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/indax.html), GENSCAN (Chris Burge,
http://gonomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Anneis thaliana"
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DAYKVLLDAFTEDEADAQSTEKNIKKEBERKKSKENSAFSRGRRKAFBETVQDEE
DDADEDEFPLKRRLESSRRGRASSSSSSSSYNNEDLKTQPEEEEDEDGVTELPPLKRY
VRRNGERGLAMTVYNNASPSSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SEHKVAAAASVELASSTSGEAKICLSFAPATGETTNLHLPSWEDLRRAMEEKCLKSYKI
VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECEISGDGWRAISNWKDITAGEENVEIPWVNEINEKVPSRFRYMPHSFYFQDAPVIFS
LESFSBDGGSCSTSCIEDCLASEMSCWONAIGVNDRFAYTLDGLIKEEFEBRISFBRDG
RKOVLRFCEECPLEBRKVEILEPOKGHLKRGAIKEOWFKCGCTKRCGNRYOVGMHW
KLOVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYORSFEDKPTLPVTLDAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGSERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVOVETPDQHYYHLAFFTT
SPIDEAMELAMDYGIDFNDNDSLMRPPCLGCSRFCRRKRSFKTMQILNKA"
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/gene"F21M11.2"
/gene"F21M11.2"
/gene="F21M11.2"
join(13061. 13488,13717. 13926,14139. 14316)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Proteins in this region are annotated in the F21M11 entry, AC002411." 1.\ 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="overlap with bases 68998-78259 of 'IGF' BAC clone
                        Buehler, E., Dunn, P.,
                                                                                                                                                                                                                                                         Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
         Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P. Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Lucs,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9893,10003. 10256,10344. .10410, [10501. .10551,10685. .10781,10885. .10913)
                                                                                                                                                                                                                                                                                                                                                                                               On Dec 30, 1998 this sequence version replaced gi:2734094.
Bases 1-926 of clone F2LM1 overlap with bases 68998-78259 of TARWY BAC clone F2DD22 (ACO002411) and bases 119525-119914 of F2LM11 overlap with bases 1-389 of 'TARWY' BAC clone F2LB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Similar to acid phosphatase; Location of ESTs 110C2T7 , gb[f42036, and 110C2XP, gb[AI100245" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Join(13061. 13488,13717. 13926,14139. 14316)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Hypothetical protein"
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/db_xref="G1:4204285"
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/chromosome="I"
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/gene="F21M11.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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FEATURES

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thale cress.

Arabidopsis thallana
Bukaryotaty, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bussicales; Brasslcaceae; Arabidopsis.
Brasslcales; Brasslcaceae; Arabidopsis.

(bases 1 to 101176)

Khan, S., Brooks, S. Buehler, E., Chao, Q., Johnson-Hopson, C., Klm, C., Shinn, P., Altafi, H., Bel, Q., Chin, C., Chiou, J., Chol, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC002560 101176 hp DNA PLN 19-JUL-2000
Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
I, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
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Submitted (25-SEP-1997) Arabidopsis thallana Genome Center,
Submitted (25-SEP-1997) University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
3 (bases 1 to 101176)
| | | | | | | | | | | | 46776 TAGCTTTCTACAAGACACTTGTACAAGACAGAGGCCA 46835
                                                                                                                                                                                                                                               1213 CTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTA 1272
                                                                                                                                                             46896 TCAAGTACACAACCAATACCAATACTTTGGCAACTGTATGGCTCCTGGTATCG
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                                                                                                                                                                                                                                                                                                        TTGGAGAAGCCATTGAAAAGAGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAA
                                                                                                                                                                                                                                                                                                                                            47016 TCACAGCGAGAATCAAAGATATGTTATCAAGCG---ATCTGTTGAAGACAGCACCAAGAT
                                                                                                                                                                                                                                                                                                                                                                                        CTTGGTTATCGGAATCTAATG3AATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGC
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                                                             CATCGAACGACGAAAATGAGCCCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTC
                                                                                                                                          T-----GACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTG
                                                                                                                                                                                                                          CAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTA
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Direct Submission
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                                                                                                                 /protein_id="AaD10670.1"
/db_xref="G1:4204289"
/translation="MNYKNELPPRRVLTADKRKERDAFISSVTDNPPEIAKFPSPPP
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KIKPSHTVEPAEECEPKRRRYREVANLLRSDGAQLPGIVNPAQLARFLK"
                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                           /gene="F21M11.7"
complement(join(29264. .31015,31312. .31414,31484. .31587,
31782. .32033))
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                          ESTS 203124T7,
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                                                        Location of Pgb|AA605510"
                                                                                                                                                                                                                                                                                                                         6.7%; Score 114; DB 12; 1
llarity 46.2%; Pred. No. 2.8e-18;
Conservative 0; Mismatches 685;
                                                                                                                                                                                                                        complement(29264. .32033)
                                                          /note="Unknown protein;
gb|H76794 and 203124XP,
                     28007. .28465
/gene="F21M11.6"
/gene="F21M11.6"
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Matches 612;
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REFERENCE

AUTHORS

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AUTHORS

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join(11965. .12033,12173. .12303,12448. .12519,12596. .12685,
12756. .12915,12985. .13041)
//note-similar to ATHP1 dbj|BAA37110.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                             VTEFTCGGFSLGIRLCHCICDGFGAMQFLGSWAATAKTGKLIADPEPVWDRETFKPRN
PPWVKYPHHEYLPIEERSNLTNSLWDTKPLQKCYRISKEFQCRVKSIAQGEDPTLVCS
TFDAMAAHIWRSWVKALDVKPLDYNLRLTFSVNVRTRLETLKLRKGFYGNVVCLACAM
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SQAKAFDERKTGVKGIVASGIKEIPAMFHTPPDTLTSLKQTAPPSQQLTIPYVDLKGG
SMDLISRRSVVEKIGDAAERWGFGVYNHGISVEVWREMKEGIRRFHEQDPEVKRFY
SRDHTRDVIYYSNIDLHTCKRAAMRDTLACYMAPDPPKLQDLPAVGGEIMMEYSKQL
MTLGEFLFELLSEALGINPNHLKDMGCAKSHIMFGQYYPPCPQPDLTLGISKHTDFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITILLQDNIGGLQVIHDQCWVDVSPVPGALVINIGDLLQLISNDKFISAEHRVIANGS
SERRISMCFCFVSTFWRRNPRITYDFISCHSELLSEQDHAKYRDLITTEFSNFFRSTFITE
SEPALFAPCFYSTFWKSPPPPKHLTITYDVBCKGASVVEKIGBAAEKWGLFHLVNHGIP
VEVLERMIQGIRGFHEQEPEAKKRFYSRDHTRDVLYFSNHDLQNSEAASWRDTLGCYT
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IGDFLQVKKIMLLLRSCFISCMIWGLILLFYCVQLITNDKFISAEHRVIANGSSEPRT
SVAIVFSTFWRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
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                                                                                                                                                                                                                                                                                /translation="mascigelhfthlhipvtinoofluhpssptpanosphhslyls
NLDDIIGARVFTPSVYFYPSTNNRESFVLKRLODALSEVLVPYYPLSGRLREVENGKL
EVFFGEEQGVLMVSANSSMDLADLGDLTVPNPAWLPLIFRNPGEEAYKILEMPLLIAQ
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Varvcisfkeccdvqnregyssnshtncdndiwhrclrclqqvdyfykmlktklqdlf
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SKFFESWDFTSDPCGFAGVYCNGDKVISLNLGDPRAGSPGLSGRIDPAIGKLSALTEL
SIVPGRIMGALPATISQLKDLRFLAISRNFISGEIPASLGEVRGLRTLDLSYNQLTGT
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FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
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/note="similar to protein kinase pir||A57676; similar to
ESTS gb|A1993651.1, dbj|AV538995.1, dbj|AV522524.1, and
dbj|AV538995.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(6700. .7357,7482. .7884,8620. .8839,
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/note="unknown protein; similar to ESTs gb|T04168.1,
gb|T21964.1, and gb|AW004462.1"
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    /note="hypothetical protein"
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                                                                                                 /evidence=not_experimental/product="F21B7.2"
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Submission

NI Submission

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YCVDALTLENKFSVLTYPPPOPVRGGTTRVNVGYGPMAVGPRMLAYASKSSKTWAVGLANGY
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KVEPIQWWDVCRRSDWLETEERLPKSITEKQYDLETVSNHLTSHEDACLSLDMNSFFS
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INCHSKPGSIESAESSEEGSTKOMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
ANGWMEKPVTAKLSTLKETRITNGFTTPPILLTDSVNEOMLSTGKPPMGFGFALHEEHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R., Shinn, P. Brooks, S., Buehler, E., Chao, O.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C.,
Chio, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,
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Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,
Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,
Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission 2000) Arabidopsis thaliana Genome Center,
Bepartment of Biology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, PA 19104-6018, USA
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                                                                                                                                                                                                                               Direct Submission
Submitted (26-JAN-1998) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
5 (bases 1 to 101176)
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                                           Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 101176)
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Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center,

    .101176
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/chromosome="1"

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                                                                                                                                                                               Ecker, J.R.
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KEYWORDS
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PONIVCGHTLTAVFVNNSHOLILEGGSTTAVANHNSSLPEISLDGVTNSVHSFDVLTR
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GGETPSPRYGHVMDIAMLVIFSGONEILDDTWALDTROFFSMDRLAPESGNQPS
GRMYASGSSREDGIFLLCGGIUHSGYTLGDTYGLKMDSDNVWTPVPRAPAPSPRYQHTA
VFGGSKLHVIGGILHRARLIDGEAVVADTNOPETSASGANRQNQYQLMRRCHHAAASF
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ISPSIGSLPELSNLILCHNHLTGSIPPFLSQTLTRIDLKRNSLTGSISPASLPPSLQY
LSLAWNQLTGSVYHVLLRLNQLNY LDLSLNRFTGTIPARVFAFPITNLQLQRNFFFGL
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WRG"
                                                                                       complement(join(18462...18515,18612...18742,18840...18975
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21929...22025,22408...22502,22866...22659,22810...22888,
23041...21301,23206...23315,23411...23556))
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                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 109.2; DB 12;
ilarity 44.9%; Pred. No. 4.6e-17;
Conservative 0; Mismatches 708;
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Best Local S:
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Patent: WO 0032789-A 40 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); CPRO DLO (NL); CPRO DLO (NL); TUNEN ARJEN
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Sapindales; Rutaceae; Citrus.
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Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and
                                                                                                                        TTACAGAGC-----AGTCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTCTAG
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MTO24
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory, Spermatophyta; Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Pl, TAC 2 (bases 1 to 82360) Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S. Direct Submission 1090 TTGGATCCTCCAATTCCACTTAATTATTTTGGTAACTGCAATGGGAGACATTGTGAGACT 1149 1207 AGTGATATGGTCAAAGGGATCGATGCGGATGCCATTGAAGCCAATGATGATAAGGTTTCA 1266 GTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAG 1337 TIATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTAAG 1217 TTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCT 1277 3, Pl clone: MT024 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl ATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAGG 1396 Submitted (13-OCT-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) structural analysis of Arabidopsis thaliana chromosome 3. II Sequence features of the 4,251,695 bp regions covered by 90 and BAC clones GTCGTATCAGAGGAA 970 GTGTTTGTTTGCATGGCTAAAGCTAAATTAGCCAAAAGCCAAAACTGAAGCTGAAGCTGCA 1030 GCAGGTAATGATGAAATTAAAAATATTATTGTGGGATTCACTGCGGATTATAGGAGCCGT CTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCAAAA GAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTGG TCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTT GCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGA clone:MTO24. Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sp Magnoliophyta; eudicotyledons; core eudicots; Rosidae; AP000606 82360 bp DNA PLN Arabidopsis thallana genomic DNA, chromosome AP000606 BA000014 Brassicales; Brassicaceae; Arabidopsis. GTATGGACATGCATGGTCAAATCAAAGATGAC DNA Res. 7 (3), 217-221 (2000) 20363099 AP000606.1 GI:6045161 (sites) 11. DEFINITION AP000606/c 978 1038 1098 1158 1267 1278 1338 ORGANISM 1218 AUTHORS TITLE REFERENCE AUTHORS 870 918 TITLE JOURNAL 1327 ACCESSION VERSION KEYWORDS SOURCE REFERENCE JOURNAL MEDLINE COMMENT RESULT LOCUS q q g g OD ò QQ δý q ò q οy g ŏ à ò ŏ

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FCRNEGWGRYFEDYMLGTISHTVNHPRGSVTNHEKYWSVLGFCLPRELLAFAIPOL
RETFMEDIAGADEGCPRMCKVRFKKNHLKGFPLDTIYAELGITQRRKESRLIRFDEIY
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KHQEWVRNYIHHIGSISRLPSCIYLLSHGETDRRSVRPNGDSMDNQRESPRWEPMDKT
DVGHASKPKADGRRISWASLR"
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NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MWEI3 and the 3' clone is Ti3J10.
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LLSIIETLRQSPREISKNDLDGACGLLRSMKEAGFKLDWLEKKLNEVLEKKEKEESYE
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    82360
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RGKREAANDIRGTPEEGFRFVDYYMYMLQKMNHESGSYVEVDEENKFNYLFFALGSSI
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                                                                                                                                              /translation="MKRNVDETSTKLKVSYFPFSFQGRKLRPNYIRDNEDLECYFEDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGACATCAAGAAGCTA---CGTGAACGAGTGGAGACCGAGTCACGCTAAGCAGCTCC 15760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15876 TGTTTCCTTCCAAAATAATTGGATCCGATATTCTCCGAGTCACGTACCGGTTAACTCGAG 15817
                                             to Mutator-like transposase
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               .50400,50660.
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                                                                                                                                                                                                                                                                                                                                                                                                                         CTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16212 CCGGAGATGAACCTCGTCCCGCCACGGAGTTTCATTCTTTAGTCCCTGAGTTACC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GGTTTCCGAGGAATCAGCTCGCGTTCTCGCCGTTCAGGTAACGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 GCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTG
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               .49959,50068.
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Pred. No. 1.7e-07;
0; Mismatches 627;
                       50779. .50980)
/note="contains similarity
gene_id:MTO24.13"
/evidence=not_experimental
                                                                                             /evidence=not_experimental
/protein_id="BAB01196.1"
/db_xref="G1:11994167"
                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
             .49683,49880.
                                                                                                                                                                                                                                                                         /note="gene_1d:MT024.14
unknown protein"
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llarity 46.2%;
Conservative
             join(49318.
50779. .509
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898 ATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTA 957
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Arabidopsis thaliana chromosome 1 clone IGF-F27B9,
IN PROGRESS ***, 5 unordered pieces.
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ACO74226
ACO74226 AL1064 bp DNA HTG 15-SEP-2000
ACO74226 AL1064 bp DNA Arabidopsis thallana chromosome 1 clone IGF-F27B9, *** SEQUENCING
IN PROGRESS ***, 5 unordered pieces.
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is record will be updated with the finished sequence soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341064
                                                   14022: contig of 14022 bp in length
14072: gap of unknown length
35113: contig of 21041 bp in length
31163: gap of unknown length
86858: contig of 51695 bp in length
86908: gap of unknown length
170536: contig of 83628 bp in length
170586: gap of unknown length
170586: gap of unknown length
341064: contig of 170478 bp in length.
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                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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Asamizu, E., Sato, S., Kaneko, T., Nakamura, Y., Kotani, H., Miyajima, N. and Tabata, S. Sato, S., Kaneko, T., Nakamura, Y., Kotani, H., Miyajima, N. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 5. VIII. Sequence features of the regions of 1,081,958 bp covered by seventeen physically assigned Pl and TAC clones DNA Res. 5 (6), 379-391 (1998)
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MXF12
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids
Brassicales; Brassicaceae; Arabidopsis.
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ATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTA
                                              -----GTGACCCGACCCGGTTTGTGTGCGTTTGG
                                                                                              CAGCGGGATTGCCGAGGACITCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTC
                                                                                                                                          65883 CATCAGACTTTCGGTCACGGTTAAACCCTCCGTTACCGCCGACGTTCTTCGGGAACTGCA
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Nakamura, Y.
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KEYWORDS
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17337. .17461,17541. .17640,17803. .17974,18073. .18191,
18285. .18395,18488. .18632,18712. .18844,18934. .19009,
19222. .19297,19385. .19492,19591. .19698,19873. .20070,
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GTGLATFVVVLMLWMRQMKRKNRKERRVVMFKKLLNMYTYAELKKITKSFSYIIGKGG
FGTVYGGNLSNGRKVAVKVLKDLKGSAEDFINEVASMSQTSHVNIVSLLGFCFEGSKR
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ONTLLJGDUCDRVSDFGLAKLEKRESVELMDTRGTIGTIATBEVESMYGRVSHKSD
VYSEGMLVIDMIGARSKEIVETVERASSYYFPDWIYKDLEDGEQTWIFGDEITKEEK
EIAKKMIVVGLWCIQPCPSDRPSMNRVVEMMEGSLDALBIPPKPSMHISTEVITESSS
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                                                                                                                IVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
ISEFLEHGSLDQFISRNKSLTPNVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKPQN
                                                                                                                                                                                                       ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRAYGGISHKSDYY
SYGMLVLDMIGARNKVETTTCNGSTAYFDDMIYKDLENGDQTWIIGDEINEEDNKIVK
KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MICFILEVERSIVSVSATAPYKDDDVFLINCGETDVPFDNHGRT
WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
RLYFYPTSYKSGFDAVNSFVSVTVNDFTLLQNFSADLTVKASIPESKSLIKEFIVPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYSTCRMMGNAQDTYLNLNFNLTWLFTVDAGFSYLVRLHFFEKYLNKANQRVFSIFLG
NQMAREEMDVIRLSGGPRIPIYLDFRIYVGSESGPRPDLRLDLHPLVKDNPEYYEAIL
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SYFETFMSEEGFLAAARMVSDSVEALDENVALKIPEILEGFTTLSPGTQVLSVAGSTR
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VHRLNVGGHMVDEVNDSGMFRRWLSDDYEFLIGGVSPYMPDVNISYTEKTPAYVAPAY
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                    SGVEILKLNDSDGNLARPNPELLVSTDSTPDDSNVTPPIKGKPHVLVIILIVVGSVIG
                                                                  LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQYIYAELKKITKSFSHTVGKGGFG
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/protein_id="BAB10829.1"
/db_xrefe"G1:10177550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="receptor protein kinase-like protein"
/protein_id="BAB10827.1"
/db_xref="G1:10177548"
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/note="gene_id:MXF12.8"
/codon_start=1
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join(25348. .26359,26401. .26756)
/note="gene_id:MXF12.7"
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/codon_start=1
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/note="gene_id:MXF12.5"
                                                                                                                                                                                                                                                                                                                                                           QEAEKQTQTLDSTII"
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Genes with similarity to proteins in the databases are described in protein of the databases are described in protein similarity are described as 'unknown protein.'

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and splicePredictor (Volker Brendel, Stanford University, http://gremlin.zool.lastate.edu/cgi.bin/sp.cgi).

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.

The 5' clone is KISE6 and the 3' clone is KAR3.
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/protein_id="BAB10841."
/db_xref="GI:10177545"
/translation="MIRHALLIFSILVSTPIVGEGATSTYEPTDVFLENCGDTSNNVD
VSGRNWTABNOKILSSNLVNASFTAGASYOESVOADIPVATARIERSEPTYSEPTTGE
SNELRLYFYPTRYGGORNAKSFTSVKVNGFTLLNNFSADLYWASKPOTEFTIKEFI
IPVYQTLNLTFTPSLDSLAFVNGIEIVSIPNRFYSKGGFDDVIINVGSSVDFHIENST
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PDDVYATSRSMGNADHPEQNLNFNLTWLFTVDAGFSYLVRLHFCETLSEVNKEGGRVF
SIFIENQTATLEMDVFRMSGGSWIPMYLDYTVIAGSGSGRRHDLRLDLHPLVSINPKY
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SLVILAMEVVGVLVINKKKSKPSYRSNRSWPCHPGTDSTNTKRAKSHPDLCKRFSI
FEIKSATNDPEDKLIGVGGFGSVYKGQIDGGATLVAVKRLETTSNQGAREFEELEM
LSKLRHVHLVSLIGYCDEDNEMVLVYEYMPHGTLKDHLFRRDKTSDPPLSWKRRLEIC
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SNYRRGTVDQIIDSDLSADITSTSLEKFCEIAVRCVQDRGMERPPMNDVVWALEFALQ
LHETAKKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
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NWTVERSQLJLSSNLVNASFFTSEASKOKAGVSBTPYMKARIFRSEFFYSFPVTPGSIF
LRLYFYPTOYKSGFDAVNSFFSVKNGFTLLRNFNDASTPQASIPLLSNSLIKETIPY
HQTLNLTFTPSKNLLAFVNGIEIVSMPDRFYSKGGFDNVLRNVSSDVDFQIDNSTAFE
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VYATSRLMGNSSNLMFNLTGMFLIVDAGYNYLVRLHFCETLPQVTKAGQRVFSIFVED
KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTNQTYYDAIL
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GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
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/protein_id="BAB10826.1"
/db_xref="GI:10177547"
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/protein_id="BAB10825.1"
/db_xref="G1:10177546"
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/note="gene_id:MXF12.4"
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/note="gene_id:MXF12.3
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2613. .5234
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/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="MXF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; admonlophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

    (bases 1 to 136047)

                                                                                                             Lin, K., Kaul, S., Town, C.D., Benito, M., Creasy, T. H., Ronning, C.M., Croo, H., Wili, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M. Arabidopsis thaliana 'IGF' BAC'FP7' genomic sequence near marker
                                                                                                                                                                                                                                                                                    Town,C.D. and Kaul,S.

Town,C.D. and Kaul,S.

Town,C.D. and Kaul,S.

Direct Submission

Submitted (01-JUN-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org

On Jan 19, 2001 this sequence version replaced 91:12280790.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28857 CGGTTCTTTCTTTGCAAGTCACTTTGTTCCCCAACCAAGGGTTTTGTATTGGTATCGCTT 28798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 TICTIGAAAIGITCICTAGAITIGGAAGCAAACCCCCTCGAITCAACAAGGIACGAGCTA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640 GATCGATAATCAAAGATCTGTATGGCCTAGAGGAAACATTTTGGAACGAAATGCAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 CGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCATAGCCGTGGCTCTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 520 CACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCATCAATGCTTGGGCCTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28683 GTACGGTTATCAATGTCCCTGCAAGTCTTGATGCAAAAATCATTGAACTTTTGTCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 GATCCGAACCGACAATACG&GTAAACGACGTTCACAATGACGTGTGGATACGTATGGACAT
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Pred. No. 3.2e-05;
0; Mismatches 520; Indels
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100215: gap of unknown length
112625: contig of 12410 bp in length
112675: gap of unknown length
116686: contig of 9853 bp in length
116686: gap of unknown length
116696: gap of unknown length
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/db_xref="taxon:3702"
/chromosome="1"
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Best Local Similarity 45.1i
Matches 436; Conservative
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112624
112674
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AUTHORS
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IFYRINVTRPFDSYTYPNIKTSLSSCLSHYLPLAGKLIUREPLDHKFTIVYSQNDDV
SFSVAETINVTRPFDSYTYPNIKTSLSSCLSHYLPLAGKLIUREPLDHKFTIVYSQNDDV
SFSVAETINADFSSLSGNEPFSTELF PULVPLQSSDDSASIVSFOYLLFPNGFCTGV
SAHHAVLDGKTTTMHEKSWAHTCKHOPFSLPODLIPTYDRTVIKSPTDSENKYLNENR
SFTKILAGGKEPANPKSLKLNPSFEIGPDVNRYTLOLTREDIOTLRERLKREVSSSS
STSSKELKELSTFVIVYSYYLVCITRAGGEPHRYOKAFSVOCKSLMNPPTNYFGN
ILVSGSNRFGVYELDFGWGRPDKVMVVSISFGNGISMAESRDONGSVEIGFSLKKHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1128 AAAGGCGTTCTTGCAGATGCAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAA 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                         /evidence-not_experimental
/product-*anthocyanin acyltransferase-like protein"
/protein.id="BAB10830.1"
/db_xref="G1:10177551"
                        /product-"transposase-like protein"
complement(join(30804. 30874,30947. 31289))
/note-"contains similarity to Ac-like transposase
gene_la:MXF12.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 66237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana chromosome I clone IGF-F7F7, PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64.2; DB 12;
Pred. No. 1.4e-05;
0; Mismatches 223;
                                                                                                                                                                                                           /evidence=not_experimental
                                                                                                                                                                                                                                       32432. .33823
/note="gene_1d:MXF12.10"
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HTG; HTGS_PHASE1.
thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTLIDLLHCELTI"
34363. .35709
                                                                                                                                                     /codon_start=1
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Best Local Similarity 49.4%;
Matches 222; Conservative
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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ORGANISM

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The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GRNSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and Splicepredictor (Volker Brendel, Stanford University, http://wremlinl.zool.astate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/cddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is T13110 and the 3' clone is T26G12.
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EEKDYARTITLPPAKEIDNDVVRVTLELTEVDIEKIKERAKNESTRSDLHLSTFVVSY
SYLTCCMYKSCGGDANRPVRMYADENRLDPPVPLTYFGNCVLPIDFNGYKATFL
GKOGYVNGYEILSDSVNGJGSRNIESIMEVYEDGTKNMKLDTQNVYVTGSNOFGIYGS
DFGWGRPVKTDVMSLYKNNEFSMSARRDEIGGLEIGISLKKCEMNVFLSLFTSDFDIY
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FMEEKGFVTAAEIISDLVKGLSSRKIETIADTFVEGFSFQSWSTQFGTIAGSTRLGVY
EADFGWGRPVKVDIVSIDQGEAIAMAERRDESGGVEIGMCLKKTEMDSVVSFFNNGLH
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KLTESSRDSFFSSILPKLEQSLSLVLSHFLPLSGHLKWNPQDPKPHIVIFPKDTVSLT
VVESEADFSYISSKELRLETELRPLVPELQVSSDSASLLSLQITLFPNQGFSIGTTVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MTLHVIETARVTPTDYSVINSANLHKLPLTFFDLPWLLFOPVKR
VFFYELTESTRDHFHSIILPKLKDSLSLILRNYLPLTGHITWEPNEPKPSIIVSENGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAHHAVLDGKTSSTFIKAWAQICKQELQSMPENLTPSYDRSLIKYPTYLDEKMIELV
RSLKEDQTNIRSLTSLPSSKLGDDVVLATLVLSRADIERLREQVKNVSPSLHLSTFVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains similarity to TNP2-like transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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acyltransferase/benzoyltransferase-like protein"
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/product="anthocyanin 5-aromatic
acyltransferase/benzoyltransferase-like protein"
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/note="contains similarity to unknown protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence-not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MOD1"
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2123. .8637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15142. .16497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="gene_id:MOD1.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (18639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emb|CAA16722.1
gene_id:MOD1.2"
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/add_graph.cgi?c=MODI
for the similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (sites)
Asamizu,E. and Tabata,S., Nakamura,A., Asamizu,E. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 85690)
Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB028618 85690 bp DNA PLN 27-DEC-2000
Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MOD1
AB028618 BA000014
                                                                                                             GCCAACGCGTATCTTTGGACATGCTTGGTAAAGACGCGTGGAGGA--GATGAGAACAGAC
                                                                                                                                                                                                                          28386 CGGTCCGTTTCATGTATGCTGCTGATTTCAGGAACCGGTTAGATCCACCGGTTCCTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATGGTCAAATCAAAAGATGACGTCGTATCAGAGGAATCATCGAACGACGAAATGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28087 TTCGGGTGGGGAAAACCATGTAACAGTGAGATTGCGTCCATTGACCGAAACGAGGCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTGATTCAGTCCAGGGATTTTGAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1359 ATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAGGCTTTTGCTCTTTGTCATAGTCT
                                                                                                                                                                                  940 TCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTA
                                                                                                                                                                                                                                                                                                                         28326 TGTATTTCGGGAACTGCGTGTTCCCGATAGGTTGCTTTGGTTACAAGGCGAATGTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTG
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DNA Res. 7 (3), 217-221 (2000)
20363099
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AB028618

QQ

ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE REFERENCE AUTHORS TITLE JOURNAL

COMMENT

JOURNAL

CDS

CDS

CDS

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YGTIPQGEVLFTHSDRTVINVSVGLEFKILQLLSYLSGDVDNDTRTLKSPSAKEIDDD
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FMYAADFRNRLDPPVPLTYFGNCVLPIDIHFGRRWVCEWRGDSK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1199 GATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGCGAAAGCCTGC 1258
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                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
complement(id109. .47990)
/note="contains similarity to reverse transcriptase
gene_id:MOD1.13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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                                                                                                                      44134. .44573
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unknown protein"
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                                                                                                                                                                                                                                                                                        /psendo
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EGTKNMKVGTKVLTVTGSNQFGIYGADFGWGRPVNTDVMSLYKNNSFSMSARRDEIGV
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EEMQKELKARHARIVNVSKVLFRNPMAPKR"
COMPLEMENT (1904) (33460. 33573, 33657. 34016,34094. 34255, 34330. 33570,33573,33557. 36093,36146. 336256))
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YNEDVQARMEAPNEEEVPTAVGPGDPTLVDVMEKLHSINDKLNEALLVLMEIEEKQAT
FEAFMDEMKAKMSQNPPDEEESTIKENAAAPVVPKRVTRSTRAKSSNV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLSTFVVTYEKSSGOSLFCKEEAKKSL"
complement(join(40204. .40603,40656. .40872))
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join(32547. 32726,32904. 33122)
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unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                             SLKRCEMIVFLSLFSNGFDN"
29217. .31674
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Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; gentiana triflora; Petunia hybrida; Petilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Aromatic acyl transferase.
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95JP-0067159.
95JP-0196915.
 96WO-JP00348
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17-FEB-1995;
29-JUN-1995;
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Mouse Wnt-3a gene.

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                                                                                                               Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
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                                                 coding for aromatic acyl transferase - for transforming h produce anthocyanin pigments and thus altering colour of flowers
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Ashikari T, Fujiwara H, Fukui Y,
Nakao M, Tanaka Y, Yonekura K;
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990S-0142154.
990S-0142055.
990S-0142390.
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99US-0151438.
   23 - JUN - 1999;

28 - JUN - 1999;

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      Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990x-0154779.
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    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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99US-0141287.
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990S-0143542
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99US-0144331.
99US-0144332.
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99US-0140695
99US-0139492
            18 - 70N - 1999;

19 - 70N - 1999;

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 57418
              1375 TTGGAGAAAGATAAAGAGTT 1394
                                  990S-0135124.
990S-0135353.
990S-0135629.
990S-0136021.
990S-0136392.
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99US-0137724.
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99US-0137222
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TTTGATGGAATGGTGTATTTGTACCAAGGCAAAATGGAGGAAGAAGAAGCATTGATGTGGAG 1344
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                                                                                                       294 gaceteactgeteceaaggaceceaacgagacetecaaeggegaa---gatgetgecaat 350
                                                                                                                                                             ccgacggtggaaccgccgcagctagtagaaaagatcttcaggttctcggactttgctgtc 410
                                                                                                                                                                                                                411 cacacgatcaagtcaagagctaattcagtaatcccatcggacagttcaaaaccattctca 470
                                                                                                                                                                                                                                                                                             984
    gacgggacatccacgtggcattttatgagctcatgggccgagatctgtcgtggagcccaa
                                          814 GACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAG------ACGCCATTCTCC
                                                                                                                                                                                                                                            ACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCAACTCAAG
                                                                                                                                                                                                                                                                  471 acattccaatccctgacatcacacatctggcgccacgtcaccttagcgcgtggactcaaa
                                                                                                                                                                                                                                                                                            CCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATCCTCCA
                                                                                                                                                                                                                                                                                                                                                  ATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACCGCGGCAGGT
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                                                                                                                                    CCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCGAGTTAGCAATT
                                                                                                                                                                                                                                                                                                            651 ctactagcagcgcacggaccggagttcggagcttcggtgatccagaaagcaatcgcggca
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Pred. No. 5.1e-83;
0; Mismatches 292; Indels
990S - 0148684
990S - 01491368
990S - 01491368
990S - 0149125
990S - 0149123
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990S - 0149123
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65.8%;
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99US-0161920.
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99US-0161993.
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23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
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20-SEP-1999;
22-SEP-1999;
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31-AUG-1999;
01-SEP-1999;
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CAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTTGGAAGTTCGCCAAGGTTCAAGGTT 1224
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                                                                                                      1045 TTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGATGATACAACAAGGGATCGTGAAG 1104
                                                                                                                                                                                                                                                                                                       TACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGAACAATAGG 1284
      534 ccggaggacataactattctcaccgtcttcgccgactgtcgccgccgcgttgatcctcca 593
                                                     cacgacgcgagtgttatcgacgcgcgtaacgacgagtgggagaaatcaccgaagattttt
                                                                                                                                                                                                                                                         985 ATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACGGGGGGGT
                                                                                                                                       654 ctactagcagcgcacggaaccggagctcggagcttcagtgatccagaaagcgatcgcggca
                                                                                                                                                                       CATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCCGAAGATCTTT
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990S-0130449.
990S-0130510.
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990S-0131449.
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99US-0132407
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05-MAR-1999;
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23-MAR-1999;
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01-APR-1999;
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-APR-1999;
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0; Mismatches 297; Indels
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22 - Jul. 1999; 23 - Jul. 1999; 23 - Jul. 1999; 24 - Jul. 1999; 25 - Jul. 1999; 27 - Jul. 1999; 27 - Jul. 1999; 27 - Jul. 1999; 28 - Jul. 1999; 29 - Jul. 1999; 29 - Jul. 1999; 29 - Jul. 1999; 29 - Jul. 1999; 20 - Jul. 20 - Jul	21-0CT-1999; 21-0CT-1999; 21-0CT-1999;
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778 aaagcaggaggcataagtattgatgtggagataactcttgaagcttctgttatggagaag 837
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                                                                                                                                                                                                              metabolic pathway; promoter; termination sequence; ss
                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 58217
                                                                                                      BP.
                         1375 TTGGAGAAGATAAAGAGTT 1394
                                                                                                    AAC48640 standard; DNA; 1364
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9905-0130891.
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                                                                                                                                               18-OCT-2000 (first entry)
                                   838 cttgtgaagagcaaagagtt
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                                                                                                                                                                                         0; Mismatches 284; Indels
                                                                                                                                                                     Score 361.6; DB 21;
Pred. No. 1e-78;
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65.6%;
990S-0160815.
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990S-0161404.
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990S-0161360.
990S-0161360.
990S-0161361.
990S-0161363.
                                                                                                                                                                                         Matches 564; Conservative
                                                                                                                                                                              Similarity
           22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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GGAAGGGCTTCATCGCCCTCTTCTAGCTGTGCAGCTCACCAAGCTCAAGGACGGGCTCAC 542
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13-AUG-1999;

16-AUG-1999;

16-AUG-1999;

20-AUG-1999;

20-AUG-1999;

23-AUG-1999;

23-AUG-1999;

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31-AUG-1999;

31-AUG-1999;

32-SEP-1999;

33-SEP-1999;

34-SEP-1999;

34-SEP-1999;

35-SEP-1999;

36-OCT-1999;

66-OCT-1999;

66-OCT-1999;
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13-0CT-1999
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99US-0145913.
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99US-0145919.
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99US-0143624.
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16-JUN-1999;

18-JUN-1999;

23-JUN-1999;

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28 - JUL - 1999
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19-JUL-19
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TGATGAAGAAGCACCACAAATTGCAGGACTTGATTCCTTGTAATAAAATCTTGAATTT 482 Gaps 6 Length 1364; Score 140; DB 21; Length 13 Pred. No. 1.1e-24; 0; Mismatches 500; Indels 9905 - 0151065 9905 - 0151065 9905 - 0151303 9905 - 0151303 9905 - 0151303 9905 - 0151303 9905 - 0152363 9905 - 0152363 9905 - 015479 9905 - 0155139 9905 - 0155139 9905 - 015659 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 9905 - 0156458 99US-0160741. 99US-0160767. 99US-0160768. 9905 - 0160770 9905 - 0160814 9905 - 0160815 9905 - 0160981 9905 - 0160981 9905 - 0161405 9905 - 0161405 9905 - 0161359 9905 - 0161350 9905 - 0161350 9905 - 0161351 9905 - 0161351 9905 - 0161351 8.7.8; 48.0%; 99US-0148565. 99US-0148684. 99US-0149378. 99US-0149425. 99US-0149723. 99US-0149723. 99US-0149930. 99US-0150565. 99US-0150884. 990S-0159331. 990S-0159637. 990S-0159638. 990S-0159584. 99US-0149902 Best Local Similarity 48.0 Matches 469; Conservative

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990S-0123180
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990S-0126248-
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990S-0126449-
990S-0130449-
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990S-013048-
990S-013248-
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CTCAGGAGAGGCCCATTCTCCACATCCAATCACTCCGCACACGTGGGCTAGCCGT
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                                                                 CTCGTGGTCCGAGCTTTGCTGTGGGTCCACCTCAATTTCTGTCCCACCATTCCTTGAACG
                                                                                                      AACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTCAAACCATCAGATGCACCGGA
                                                                                                                                           ACATGCTAAGTCAGCAACCAACGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGA
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                            CATGGGATTAGCATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACTTTATGAC
                                                                                     cgcatggtccgaaatcttccaaggacaagagagacaaccaaaacgatgacttgtgtcttaa
                                                                                                                         gaatccacccgtgttgaagcgttacatccctgaaggatacggtcctctattcagccttcc
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

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ATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAGAAGTTGCAGATCTTACT 423
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0; Mismatches 134; Indels
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  990S-0151433.
990S-0151930.
990S-0153163.
990S-0153758.
990S-0154018.
990S-0154779.
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9903-0157753.
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990S-0158029.
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990S-0159369.
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99US-0160741.
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990S-0161404.
990S-0161405.
990S-0161406.
990S-0161359.
990S-0161361.
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99US-0159331.
99US-0159637.
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99US-0160814.
99US-0160815.
99US-01609E0.
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Best Local Similarity 62.5%;
Matches 283; Conservative
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99US-0161993.
99US-0162142.
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01-SEP-1999;

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   GATGAAGAAGGCACCACAAATTGCAGGACTTGATTCCTTGTAATAAAATCTTGAATTG
                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                               GAAGGGCTTCATCGCCCTCTTCTAGCTGTGCAG 516
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Pred. No. 9.6e-23;
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Best Local Similarity 46.8
Matches 488; Conservative
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    Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 34861.
                            AAC42254 standard; DNA; 1520 BP
                                                                                                                                                                                                                                                                                                                      990S - 0121825
990S - 0123180
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                                                                                1201 cggctcatcaagacgggaggattcgtagcgttgtggcggattgggaagcgaatcccaggt 1260
                                                                                                         1160 TCTTTCAGTACAAAGATGCTGGAGTGAACTGTTGCTGTTGGAAGTTCGCCAAGGTTCA 1219
                                                                                                                                                                                                                     ATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTGATG 1339
                                                                                                                                                                                                                                    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
1040 CAGGTTTGTTACTAGCAAGCCCGGATCGAGTTCGCTGGTGGGATGATACAACAAGCGATCG 1099
                         1141 cggcagaggttttgtcacgtgatcttaaatggtgcgctgatcagcttaaccagagtgttg 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                           1100 TGAAGCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCCGAAGA
                                                                                                                                                                              AGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGAACA
                                                                                                                                                                                                                                                                           1340 TGGAGATTAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGAAAGATAAAGAGTT 1394
                                                                                                                                                                                                                                                                                         Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 106.2; DB 21; Length 1520;
49.9%; Pred. No. 2e-16;
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990S-0161406-
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990S-0150884.
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99US-0161404
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Matches 267; Conservative
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25-0CT-1999;
26-0CT-1999;
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28-OCT-1999;
29-OCT-1999;
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27-AUG-19
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28-SEP-1
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Example 6; Page 127; 159pp; English.
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                                    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                              TGGGAGAGCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTT 1200
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Conservative 322; Mismatches 197; Indels
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                       5.0%; Score 81; DB 22; L ilarity 1.1%; Pred. No. 2.3e-10; Conservative 322; Mismatches 197;
                                                                                                                                                                                   Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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                                                                                                                                 monitoring gene expression
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Conservative 322; Mismatches
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                                                                         (CLIN-) CLINICAL MICRO SENSORS INC
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gene expression; ss.
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nilarity 1.1%; Pred. No. 2.3e-10;
Conservative 322; Mismatches 197.
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1.1%; Pred. No. 2.3e-10;
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                                   ETM; mismatch; genotyping;
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                                                                                                                       AAF58262 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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                                  1381 AAAGATAAAGAGTTCCTCATGGAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTA 1440
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Search completed: November 5, 2001, 18:11:37 Job time: 15432 sec

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AB026495 Petunia x
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AB008264 Arabidops
AL137189 Arabidops
AB002499 Arabidops
AL133421 Arabidops
AF002109 Arabidops
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               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                              1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
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AP002842 Oryza sat AJ310831 Medicago AL132976 Arabidops I66494 Sequence 14 AB020742 Arabidops AP003279 Oryza sat	AP003442 Oryza sat AX025514 Sequence E10125 DNA encodin E10126 DNA encodin AL42115 Oryza sat MIGA5 D. Giscoideu AL08970 Plasmodiu AL4008970 Plasmodiu AL40348 T3 end of AE001373 Plasmodiu AE001373 Plasmodiu	AP002460 Arabidops AP000606 Arabidops AC074226 Arabidops AC074229 Plasmodiu AP351290 Plasmodiu AL356372 Homo sapi AL034559 Plasmodiu M73676 Dictyostell M29237 D.discoideu AC005507 Plasmodiu AE001397 Plasmodiu	AC004710 Plasmodiu AC005507 Plasmodiu AC001366 Plasmodiu G3798 GARP Plasmo J03998 Plasmodium AF088979 Dictyoste AL427304 clone BA0 AF070091 Plasmodiu
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102.8 94.4 68.8 67 67 60.8	60.8 53.6 57.4 53.2 53.2 51.6 51.4 51.2	0000 4444 0000 4444 0000 000 000 0000 000 0000 000	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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CIZNI5/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                               24-JUN-1998
                                                                                                                                                                                                     Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 3 18-MAR-1997;
                                            acyltransferase, complete cds
                                                                                                                                                                                                                                                                                                                                                                      (C12N9/10,C12R1:19);
strandedness: Double;
topology: Linear;
Key
                               DNA
                                          Petunia hybrida mRNA for
                                                     E12755
E12755.1 GI:3251587
JP 1997070290-A/3.
unidentified.
                            1605 bp
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                                                                                                                unidentified
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                               E12755
RESULT 1
E12755
LOCUS
DEFINITION
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SOURCE
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1. 1605
/organism='Petunia hybrida'
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67. 1413
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                                                                                                                                     DB 10;
                                                                                                                                     99.9%; Score 1603.4; 99.9%; Pred. No. 0;
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1. 1605
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/db_xref="taxon:32644"
a 318 c 376 g 434
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Unpublish 2 (bases Tanaka, Y. Direct Su Submitted Yoshikazu Wakayama-						477 8	Sim	1 TGTCGACGAAA	TTATCCATGGC	TTATCCATGGC ACAAACGTGAA	ACAAACGIGAA CTTCCTTACCT 	241 TTTGACGAGAC 241 TTTGACGAGAC 301 CAACTAGCTGG 301 CAACTAGCTGG 301 GACATGGATGG 361 GACATGGATGG 421 ACTGATGAACA 421 ACTGATGAAGA 421 ACTGATGAAGA 421 TTGGAAGGGCT 481 TTGGAAGGGCT
JOURNAL REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUFCE	gene	CDS			BASE COUNT ORIGIN	Query Match Best Local Sir	Matches 1	9	121	Db 121 A Oy 181 C Db 181 C	Oy 241 7 Ob 241 1 Oy 301 C Oy 361 C Oy 361 C Oy 421 P Oy 421 P Oy 421 P Oy 421 P
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AACTCAGGAGGAGCCATTCTCCAATTCCAATCACTCTCCGCACACGTGTGGCTAGCC 900	TGCAGGAAAAGGGTTGATCCTCCAATGCCAGAAGTTACTTCGGCAACCTAATTCAGGCA 1020 	ATTITCACAGIGACCGCGGCAGGTIGITACIAGCAAGCCCGATCGAGTICGCIGGIGGG 1080 	ATGATACAACAAGGGATCGTGAAGGATGACGCTAAGGCCATTGATGAAGAAGAAGGAGGAG 1140 	TGGGAGAGCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTT 1200 	GGAAGTTCGCCAAGGTTCAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGT 1260 	GTGAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAAT 1320 	GGAGGAAGAAGCATTGATGTGGGAGTTAGGAAGCAAATGCTATGGAGGGGGGGG	. AAAGATAAAGAGTTCCTCATGGAAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTA 1440 	. CACTTTATTTATGAGCTGCTATGACTCACATGCATGTATTTTTTTT	TCTTTCCTTTTATTGTTTTCTTTTTCTTTCTTGTACGTTATGAAGAAACCGAG 1560 	1561 TATAAAGGAATAATGTTTTCAGTTATTAAAAAAAAAAAA	AB026495 1605 bp mRNA PLN 04-APR-2000 Petunia x hybrida mRNA for acyltransferase homolog, complete cds. AB026495 1 GI:7415598 AB026495.1 GI:7415598 ACYLtransferase homolog. Petunia x hybrida cDNA to mRNA. M Petunia x hybrida Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta eudicotyledons: core eudicots: Asteridae: euasterids I; Solanales: Solanaceae: Petunia. I sitea: I sitea: Viridiplantaex,K., Tanaka,Y., Fukuchi-Mizutani,M., Fujiwara,H., Fukul,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T. Molecular cloning and blochemical characteization of hydroxycinnammoyl-CoA-anthocyanin 3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla frutescens and diverse plant acyltransferase homologs
Oy 841 Db 841 Oy 901 Db 901	Oy 961 Db 961	Oy 1021 Db 1021	Oy 1081 Db 1081	Oy 1141 Db 1141	Oy 1201 Db 1201	Oy 1261 Db 1261	Oy 1321 Db 1321	Qy 1381 Db 1381	Oy 1441 Db 1441	Qy 1501 Db 1501	Oy 1561 Db 1561	RESULT 2 ABO26495 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE

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                                                                                                                                                                                   Research;
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1. .1605
/organism="Petunia x hybrida"
/db_xref="taxon:4102"
/note="synonym:Peunia hybrida"
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Pred. No. 0;
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7. and YoneKura-Sakakibara,K.
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67. 1412
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         ACCTCGTGGTCCGAGCTTTGCTGTGGGTCCACCTCAATTTCTGTCCCACCATTCCTTGAA
                                               661 CGAACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTAACCATCAGATGCACCC
                                                                                                                GAACATGCTAAGTCAGCAACCAACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGC
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/pvidence=not_experimental
/protein_id="mansh10046.1"
/db_xref="G1:10176840"
/db_xre
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GYVYDIRKLVDPALTLQGHTKTVSYVRFLDGGTVVTAGTDGCLKLWSVEDGRVIRTYE
GHVNNRNFVGLSVWRNGALFGCGSENNRVFVYDRRWGKPVWVDGFEPVGMNSGSDKRF
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Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned Pl clones
DNA Res. 4 (3), 215-230 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophy
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids
Brassicales; Brassicaceae; Arabidopsis.
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Direct Submission
Submitted (02-JUL-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                         5, Pl clone: MRO11
                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thallana (strain:Columbia) DNA, clone_lib:Mitsui
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    .82415
    /organism="Arabidopsis thaliana"

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2972. .4078
/note="contains similarity
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Arabidopsis thaliana genomic DNA,
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AB005244.2 GI:10176838
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join(29073. .29168, 29422. .29523, 29617. .29795, 30379. .30495)
/note="gene_id:MRO11.14
pir ||T00970
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LNIYFRDIXKPIPSTYNLVMAMLWRHPEHIDLDQISVVHYCANGSKPWKFDEAEEHMD
FREDIKMLVKKWEIYEDSSLDYKNFVETESKLAMVTATLASKKLVGDVLTSLAPSAA"
complement(join(19902. 19929, 20117. 20706, 20859. 20944,
21102. 21144, 21356. 21805, 21914. 22375))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"amino acid transporter"
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NNYFWVLFGLTQIFWSQIPNFHNWWWLSLVAAIMSFTYSFIGIGLALGKIIENKKIEG
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VVSPSVGPHENPTITINLFGSASKNIPAGTLVYVAFRDGEFTGLLKTYNLCDVSACNN
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VVKYLDDDKRWYCFESPPDINGLPFRHYLLEWYDBK1YSWYISEKKRLA
EEPPWESPGTIVELCSKRDBGEVVWVPALVYKEFKENDEYRYIVKDKPLIGRSYKSRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIRGIPAENNGEKWAIVFQALGNIAFSYPFSIILLEIQDTLRSPPAEKOTMKKASTVA
VFIQTFFFFCGGCFGYAAFGDSTPGNLLTGFGFYEPFWLVDFANACIVLHLVGGYQVY
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LRKVKSAYPLVVATLPDVPEEHRQILVDQGCIIRDIEPVYPPENTTGYSMAYYVINYS
KLRIWEFVEYEKMIYLDGDIQVFKNIDHLFDTPRGYLYAVKDCFCEVSWSKTPQYKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVMFPYFNEYLGVVGALAFWPLAVYFPVEMCILQKKIRSWTRPWLLLRGFSFVCLLVC
LLSLVGSIYGLVGAKFG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 CAGCTCACCAAGCTCAAGGACGGCCTCACCATGGGATTAGCATTTAACCATGCTGTGCTG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | GATGGTACTTCGACGTGCCCTTTTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAATTTCTGTCCCACCATTCTTGAACGAACCAAGGCTCGTAACACTCGAGTCAAGCTC
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llarity 65.8%; Pred. No. 2.9e-79;
Conservative 0; Mismatches 292; Indels 12;
                                                                                                                                                                                                                                                                                                                                           similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence*not_experimental
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                                                                                                                                                                                                                                                                                                              gene_id:MRO11.16
                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Best Local Simi
Matches 586;
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KERENDDSYKITKOKSFSCEGKKARPNKTVDLSSLRPIPVSYDEYQLEENVEYFLDG
MGWHGRYWGSQERAIGTLSOKWYFRLESTSKKQLFREKWAREGWWKLQT
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QNGSGNDSTLENENSEDNNRKRREENLGCVASVEQDKPKDTTWVLPFEKKLRIWETL
ESMEYFKYPQSPHYSPLLVESREDSREMSANGMMIFFGLLDEVKALCHNDPISFFI
SLTNSFALEKHGFNVKAPQSRINKLLSLRNGSKKTEELKDAEKVTAREKESVRAENK
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COMPLEMENT(1010(14977...15576,15706...15842,15938...16007,
16239...16713.)
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similar to unknown protein"
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8552. .8593,8938. .9139))
/note="contains similarity to remorin
gene_id:mR011.21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLPSPAPAEEKQEDSKAIVPVVPKEVEEKKEGSVNRDAVLARVETEKRMSLIKAWEE AEKCKVENKAEKKLSSIGSWENNKKAAVEAELKKMEEQLEKKKAEYVEQMKNKIAQIH KEAEKREMERREAERAMEEARKKAESTUEQUKKKAETVEQMKNKIAQIH COMPLAMENT (10928. 11128)
//note="gene_id":RR011.20
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-not_experimental
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/translation="MFSPGTTVEVSSKINNKEVVWVPAVVIKEFKEDDEYKYIVRVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSFSCKGNKAARLNKTVDLCSLRPTPPSISVEEYQLKEYVEVFHDGMGWRQGRVMKIQ
ERVMLSQGRVWYSQGRVMGNLSQKCYIVLLEATKKQISFKQSDLRPLQVWEDGVWKML
QYRESSLTGOGGGDETSDSVRANNESDPPVTPRPGTTPPLKQTAEAFGYRTLERWQNA
SYNDSTRENNSEDINKRKREESLCSDAFTTPPLEFEKKLSIRKTLESPRVQA
SPHFSPLVETREDCREMSAVGMALTFPCLLEEVKSLQHDNSISSLISLSNNFCELEKY
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13376. .13819,13934. .13957))
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complement(join(17869. .18087,18174. .18308,18396. .18719, 19960. .12283)
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                                                                                                                      /evidence=not_experimental
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/evidence=not_experimental
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/protein_id="BAB10052.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to unknown protein"
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                                                                                                /codon_start=1
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                                                                                  COMMENT
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Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                               75123 GACCTCACTGCTCCCAAGGACCCCAACGAGACCTCCAACGGCGAA---GATGCTGCCAAT 75067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                 Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned Pl clones
DNA Res. 4 (6), 401-414 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB008264 79976 bp DNA PLN 27-DEC-2000
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MBD2.
AB008264 BA000015
AB008264.1 GI:2618599
                                                                                                                                               814 GACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAG------ACGCCATTCTCC
                                                                                                                                                                                                               ACATTCCAATCACTCTCCGCACACGTGTGCCTTAGCCGTCACACGTGCGCCCCAACTCAAG
                                                                                                                                                                                                                                                                                                                                              985 ATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACCGCGGCAGGT
                                                                                                                                                                                                                                                                                                                                                                 1165 CAGTACAAAGATGCTGGAGTGAACTGTGTTGCTGTTGGAAGTTCGCCAAGGTTCAAGGTT
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                                                                                CCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCGAGTTAGCAATT
                                                                                                                                                                                                                                                                                CCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1105 CATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGGAGCAACCCGAAGATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1345 ATTAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGAAAGATAAAGAGTT 1394
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Nakamura,Y.
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VERSION
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Interconduction of Plant Gene Research: 1522-3, Yana, Risarazu, Chiba 292-0812, Japan Geme Research: 1522-3, Yana, Risarazu, Chiba 292-0812, Japan Geme Research: 1522-3, Yana, Risarazu, Chiba 292-0812, Japan Gemall:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

Address for correspondence: kaos@kazusa.or.jp For the latest information on mortation of this clone, please see http://www.kazusa.or.jp/kaos@cgi-bin/aqd_graph.cgi7c-MBD2

Genes with similarity to proteins in the databases are described in 'protein similarity to proteins in the databases are described in protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail.1.3/), GENSCAN (Chris Burge, MIT, http://ccR-081.mit.edu/GENSCAN.html), NetGene2 (5.M Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlini.acol.lastate.edu/cgi-bin/sp.cgi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAKLPRVIHVNHHDHRVSYKYPLGPGEWRCGVCWEEIDWSYGAYSCSLCPNYAMHSLC
ATRKDVWDGRELDGYLEEIEDIEPFKRNDDNTITHFTHEHNLSKDGTTLKKSILCVAC
VOLGTDTFYNCSESSCSFVLHETCANISKKRRHFLSPVPLVLCLQNQRNTETCNACQ
QVCCKGFIYSSFPKTVYREKFYDLQCSSITVPFFHGSHDHHLLFLKLKGRGNKTCECC
GIVQKEYAIGCTKCNYFLDFRCATLPLLVRLPRYDDHPLTLCYGDEKASGKCWCDICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-*MDSSSSWIVSKSFVKPKTLPEESKQPYYLSPWDYAMLSVQYIQ
KGLLFHKPPLDSIDTLLEKLKDSLAVTLVHFYPLAGRLSSLTTEKPKSYSVFVDCNDS
PGAGFIYATSDLCIKDIVGAKYVPSIVQSFFDHHKAVNHDGHTMSLLSVQVTELVDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGLSMNHAMGDGTAFWKFFTAWSEIFQGQESNQNDDLCLKNPPVLKRYIPEGYGPLF
SLPYSHPDEFIRTYESPILKERMFCFSSETIRMLKTRVNQICGTTSISSFQSLTAVIW
RCITRARRLPLDRETSCRVAADNRGRMYPPLHKDYFGNCLSALRTAAKAGELLENDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="CHP-rich zinc finger protein-like"
/protein_id="BaB09185.1"
/db_xref="G1" 9758572"
/translation="MS1FEGHEHHVSIIKHRDGLECDACDRSFGDVISCGECKFTVH
RKCVFMFDIQEIFDHPSHDGHCLKLITGAPDDTDQKCHLCGKKTKRLLYHCSDCKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASVFDSPEITHPSHVRHPLKLRSNGAPDYTNLNCHICGDATGNLLYHCDICKFNLNM
RCAIREPTPVALSNMKVHEHTLTLMPRLISFVCDACGMKGDRAPYVCVQCDFMIFHQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes encoding IRRMs are predicted by IRRMscan'SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy//RNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MJB21 and the 3' clone is MRD20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDIDCIIDYICARSPLKLPWHDHPLIKVDLGANMPCDFCNESGIDYCCPRCRFMIHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAALKVHQAVAEHTSEKVSQMIDQWLKSPYIYHIDRLFEPMSVMMGSSPRFNKYGCEF
GLGKGVTLRSGYAHKFDGKVSAYPGREGGGSIDLEVCLVPEFMEALESDEEFMSLVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="N-hydroxycinnamoyl/benzoyltransferase-like
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit."
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/product-"02 snRNP auxiliary factor, small
join(5306. .5761,5932. .6828)
/note-"gene_id:MBD2.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="CDS is reported in Acc# AB007647
gene_id:MJB21.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id~"BAB09184.1"
/db_xref="GI:9758571"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mitsui P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1. .218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MBD2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 79976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=1
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CDS

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/translation="MVGDYRGRFSSRRFSDDSDDASSVEGETTSSMYSAGKEYM
ETEWTNEKHSLYLKSMEASFVDQLYNSLGALGKNENVSESTRFGSGRKPSQEQFKVLH
DGFWQKINVKQPEHRINGRHGGNSHEFLRSPWIKHYKPLVKTQIPVTDEPENQVVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGKKGICSSGSASSLKQLSSHSRDHDQISVGEEVSDQNFVNEGIKGENGSSKKMKTVM
MSESSTDQESVGTEMEKETDQESVAIEHLQKQ"
complement(30319. .31245)
                                                                                                                                                                                                                                                                                                                                                 /translation="manTQLKSDAIMDMMKEHLSTDAGKEVTEKIGLVYQINIAPKKL
GFEEVTYIVDLKKGEVTKGKYEGGKVDATFSFKDDDFVKVATGKMNPQMAFIRGAMKI
      PEGRNKENGFGOSKSFAFGEQGSSSNNTGGSTTTNNNNLTPETKKKKKKKLSLFPKVFM
                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(25760. .25834,27425. .27528,27615. .27900,
27989. .23171,28527. .28634))
/note="gene_id:MBD2.9
pir | T05226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence~not_experimental
/product='non-LTR retroelement reverse transcriptase-like
                                                                .23461,24198. .24300,24565. .24625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5910 TCAGTCACTTGTGTTTGTGTAGGTGACAGAATTGGTAGAATTGCAATTTTCATAGGACTGTC 5969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6384 GTATCCACCGCTTCACAAGGATTACTTCGGAAACTGCCTCTCTGCTTTGAGAACGGCTGC 6443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCAACCAACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6030 AATCTTCCAAGGACAAGAGAGAGCAACCAAAACGATGACTTGTGTCTTAAGAATCCACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCATCTCATCTTTCCAATCGCTAACGCGGTTATATGGAGATGCATAACAAGGGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGCCCTCTTCTAGCTGTGCAGCTCAGCTCAAGGACGGGCTCACCATGGGATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5970 TATGAACCATGCGATGGGAGNCGGTACTGCGTTCTGGAAGTTCTTTACCGCATGGTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675 TAACACTCGAGTCAAGCTCANCCTCTCAACCATCAGATGCACCCGAACATGCTAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6090 GTTGAAGCGTTACATCCCTGAAGGATACGGTCCTCTATTCAGCCTTCCATATAGTCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCTCCGAGTTAGCAATTGACAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6204 TTTCTCATCAGAAACCATAAGAATGCTTAAAACAAGGGTCAACCAAATATGCGGAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATTCTCCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6324 GAGATTACCTCTCGATCGAGAAACAAGTTGTAGAGTTGCTGCTGACAACAGAGGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATCCTCCAATGCCAGAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 ATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACTCAAGCCCGAGGACTNCACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 79976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.1e-21;
0; Mismatches 458; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to unknown protein"
                                                                                                                                                                                             similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence"not_experimental
/protein_ld="BAB09191.1"
/db_xref="G1:9758578"
                                                                                                                                                                                                                                                    /evidence=not_experimental
/protein_id="BAB09190.1"
/db_xref="GI:9758577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 135.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="gene_id:MBD2.10"
                                                                complement(join(23380.
                                                                                             24707. .21832))
/note="gene_id:MBD2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

8.4%;

Best Local Similarity 48.5%;

Matches 439; Conservative
                                                                                                                                                             pir||T28058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495
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                                                                                                                                                                                                                                                                                                              QSWCPDCVRAEPVIYKTLEEFPEEVKLIRAYAGDRPTWRTPAHPWRVDSRFKLTGVPT
LVRWGDSVRKGRLEDHQAHLPHLILPLLAPST"
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complement(join(14641...14694,14770...14868,15144...15272,
1358...15401,15497...15569,15650...15736,15848...15972,
16050...16123,16204...16733,16863...17553,17677...18603))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVEGSSEMLVDSDSILETPLVASPTLRFLDEKEQDFRESTNVEDYCEEDGSSGVVVEN
GLEASSWPSETYSEGSGNVEIFVERFREALAEDAYGSSDLOSKQELTARPESVEIAT
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IEEEOFSFSDLDECKPGGNSSVGSSSDTVKVDGKESYDETKTSPEKGVENTMALSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIERKKDIFTDEMERLVGSLPIMRLQNNDDMDASPSQPLSQSFDPCFNTSKLDLRED
ESSSGGLDAESVAESSPKLKAFKHVIANPEVVELSLCKHLLSEGMGAEAASQAFNSEK
LDMEKFASLGPSILENDKLVVKIGGCYFPWDAAAPIILGVVSFGTAQVFEPKGMIAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNEKPGDVLAGGSGSWKLWPFSLRRSTKEAEASPSGDTAEPEEKÖEKSSPRPWKKTVR
ALTPFSEQLASLDLKDGMNSYTFTSTNIYGTQQVDARIYLMKWNSRIVYSDVDGTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELGRERQDLEETKQKESTGLARTNDKDAGEELVETAKKLEQATKEAEDAKALATASR
DELRWAKELSEQAKRGMSTIESRLVEAKKEMEAARASEKLALAAIKALQETESSQRFE
EINNSPRSIIISVEEYYELSKQALESEEEANTRLSEIVSQIEVAKEEESRILEKLEEV
RETNPKSWFYTCKDCGVTFHIFCVVWDIRFSKQGETIRDGVELLPNNTSSRPLCKNCQ
CRCLGPFFVKDYDNICYCSYYCYARLHSLRYIWSKFRCPPWISEPST*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAYYREGKPOCYLKKIRININ TRIDINGVODSCENAY LAHITGGAYFLKEVEDVEVENAY BY TLSSGDEAETTSRDDVVDKVKIPLKSRSCHYDSPSPRTGOKIVGKFOILLGYVFGG RSVRESQDCGVERAEIAADLLEVKWSTNIDTRKRGKCMSSESLDGKDYGESTSTSGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NPFQDCETSPINEPPKVYVAPRVMISHQDSFSEDSRTDVIEDARILPASPRLRVPASP
RAFVYPRSVESPRFGSPRSVESPCFGSPIGVIDTASPFESVREAVSKFGGITDMKAHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEKEEQQAKQDSELAQMRVEEMEKGVANEASVAVKTQLEVAKARQVSATSELRSVREE
IEMVSNEYKDMLREKELAAERADIAVLEAKEIERTMDGLSIELIATKELLESVHTAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTELAAFTDISSGNLLLEKNDIHAAVESARRELEEVKANIEKAASEVKKLKIIAGSLQ
                                                                                                                                                                                                                                                                                    /translation-"MTLKKVDANPSTLESSLQELKSDETSRSKINFILFLADNDPTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation*"MNAVGRIGSYIYRGVGTVSGPFHPFGGAIDIIVVEQPDGTFKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MLGDDKDSDDLNLFLNAIGEAGDEEGPTSFNDIDFLTFDDEDLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NREMSVRKAELKEANGKAEKARDGKLGMEQELRKWRSENGKRRTDEGREPEKSPTRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQTIERRKMVDEELEKIQEAMPEYKREAELAEEAKYDALEELENTKGLIEELKLELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>EAEEK RFSVAMARDQDVY NWEK ELKMVENDI ERLNQEVRAADDVKAK LETASALQHDL</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPRRCYVLAFIVGFSLLFAFFSLILYAAAKPQKPKISVKSITFEQLKVQAGQDAGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strong similarity to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strong similarity to unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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ATTGSTSGVVPDDSARRCKTDDQVHTCSNLGKYKASRDLQYSTEDQLASRDSLNKQEI
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STRTSRIPFREFEDESKRERHBSPSFKRFSFESFRCLSNRFSLKDISAGOPLSSSEDTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDISEQKSLITESVLEDESEOYKGRKEVAAVVIKKKPVEGSYTSFEETSVIIPGGVHS
FPEKGAPSPLISRWRSGGLCDCGGWDVGCKLHVLSNKTVLHKFNQSFTLFDQEVSEQD
SSPALAMTELKTGIYRVEFGSFVSPLQAFFVCVTVLTCASKAKTTGKSSSPMAPPLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKVLNKEGLQGHREWLTEVNFLGQLRHPNLVKLIGYCCEDDHRLLVYEFMLRGSLENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFRSNPRTLLHFLKMMIALGAAKGLAFLHNAERPVIYRDFKTSNILLDSDYTAKLSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARPLMSDVVETLEPLQCTGDALIPCATTTAGAAFAMGGVPDYRMHRRFAKNVGPGAIC
RSPNPNYSPGGPAACRVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSSDSSFKDDSVQYCTFYSVNEVKKKSGSWLIHGHREKHCGFVYNIIGQMQLGNSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLAKAGPQGDETHVSTRVMGTYGYAAPEYVMTGHLTARSDVYSFGVVLLEMLTGRKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKTRPSKEQNLVDWARPKLNDKRKLLQIIDPRLENQYSVRAAQKACSLAYYCLSQNPK
                                                                                                                                                                                                                                          /note="strong similarity to serine/threonine-specific
protein kinase NAK, Arabidopsis thaliana, EMBL:AL162874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity to predicted proteins, Arabidopsis thaliana"
                                                                         .2207,2629. .2752,2857. .2962,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(6055. .8082,8214. .8420)
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/note="EST F14175 marks 5' end of this gene; 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2208. .2628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3556)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains an intron
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6055. .8082
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1726. .3687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bevan, M., Zimmermann, W., Grueneisen, A., Wambutt, R., Kalicki, J., Wohldmann, P., Smith, A., Bancroft, I., Mewes, H.W., Rudd, S., Lemcke, K. and Mayer, K.F.X.
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Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Submitted (26-JUL-2000) MIPS, at the Max-Planck-Institut fuer
Buchchemin, Am Klopferspitz 18a, D-8155 Martinsried, FG. E-mail:
lemcke(@mips.blochem.mpg.de,mayer@mips.blochem.mpg.de project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
On Jul 27, 2000 this sequence version replaced gi:6759425.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
Location/Qualifiers
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Arabidopsis thaliana DNA chromosome 5, BAC clone F7J8 (ESSA
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                                                                              6444 AAAAGCTGGTGAACTATTGGAGAATGATCTTGGATTTGCTGCTTTGAAAGTGCATCAAGC
                                                                                                                                                                                                                                            1155 GAAGATCTTTCA---GTACAAAGATGCTGGAGTGAACTGTGTTGCTTGGAAGTTCGCC
                                                                                                                                                                                                                                                                                               6564 TTATATTTACCATATTGATCGGCTATTTGAACCGATGAGCGTTATGATGGGAAGCTCGCC
                                                                                                                                                                                                                                                                                                                                                        1212 AAGGTTCAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGG
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                                                                                                                                    GATCGTGAAGCATGACGCTAAGGCCATTGATGAAAGAAACAAGGAGTGGGAGAGCAACCC
                                                                                                                                                                                    2 (bases 1 to 3766)
Bevan, M., Rose, M., Hempel, S., Entian, K.-D., Bancroft, I.,
Mewes, H.W., Rudd, S., Lemcke, K. and Mayer, K.F. X.
Unpublished
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EU Arabidopsis sequencing, project.
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complement(1726. .2207)
/gene="F7J8_5"
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ALI37189.2 GI:9542859
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EQMIPTYNGSILGGPTINVREGOTLVVHVINKSTYNVTHWHGVFQLKSVWMDGANMIT
QCPIQPSNNFTYQFDTTGQEGTLLWHAHVNNLRATHGALITRPRSGRPYPPRYKE
VPLIFQQWMYTDVRLLELFRPPVSDAYLINGLAGDSYPCSKNRMFNLKVVQGKTYLLR
INAALMTHLEPKIAHNVTVVAVDAYYTPYLTDVMILTPCQTIDAILTANQDIGTY
YMAIIPYPRAIGVPASPDTKPTRGLIVYEGATSSSSPTKPWMPPANDIPTAHRESSNI
STSUGGBWHYPVPRHVDEKMPTYMGLGLIDPCRSARKKVGFLORGLAGSINNRFRBIPE
RISMQBAYFYYTDJFDQAPLKFDFTKFDGPTKFDFTKFBYPR
NSTVEIYLQGPHTGILTPESHPMHLHGFNFYVLGYGFGNYDPIRDARKINLFNPQMHNTV
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
/translation="MPRVHHSLSNQAFLVLLLFSSIASAAIVEHVLHVKDVVVTPLCK
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Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81127 TGTTTCCTCTCGGAAATCCAGATGGAGCTTCGATCACGATGGGGGGCTCGCCGAGATTCC 81186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thallana genomic DNA, chromosome 5, Pl clone:MXM12. AB005249 BA000015 AB005249.1 GI:2264321
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                                                                                                                                                                                                                                                                                                                                                                                   860 TCTCCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCCAAC 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81247 ATAAATTCGACGGGAAGATCTCGGCGTTTCCCGGTAGAAGGAAACGGAAGCGTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920 TCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATC
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                                                                                                                                                                                                                                                                                        Score 131.8; DB 13; Length 118507; Pred. No. 1.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1340 TGGAGATTAGTTTGGAAGCANATGCTATGGAGAGGTTGGAGAAAGATAAAGAGTT 1394
                                                                                                                                                                                                                                                                                                                                           0; Mismatches 252; Indels
                                                                                                                                                                                                            QCTRDPTIYDSRTTNVDMSY"
complement(13626. .13810)
/gene="F7.78_30"
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Arabidopsis thaliana
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Matches 283; Conservative
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SLVGGPHWTPVPRHVDEKMFITMGLGLDPCPAGTKCIGPLGQRYAGSLNNRTFMIPER
ISMQEAYFYNISGIYTDDFPNQPPLKFDYTKFEQRTNNDMKMMFPERKTSVKKIRFNS
TVEIVLONTAIISPESHPMHLHGFNPYVLGYGFGNYDPIRDARKLNLFNPQMHNTVGY
PPGGWWYLRFTANNGCWLFHCHMDAHLPYGIMSAFIYQNGPTPETSLPSPPSNLPQC
TRDPTIYDSRTTNIDLSY"
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COTIOPCYMPTYQFDITGQEGTLLWHANVNILAATHGALVIRREGGRPYPFPKFYKE
VPIVFQQWWDTDVRLLGPPPVSDAYLINGLAGDSYPCSENRWFNLKVVQGKTYLLR
IVNAALNTHEFRIAHRNVTVVAVDAYYSTPYLIDVMLITPGGTVDALLTADQALGKY
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15387, .15631,15775, .15926,16131, .16229))
/gene="F7J8_30"
                                                                                                                                                                                                                                                                                                                                                                                   /product-"laccase-like protein"
/protein_id="CAB69812.1"
/db_xref="G1:6759427"
/tanslation="MPRLHHYLSNQAFLVLLLFSSIASAAVVEHVLHIQDVVVKPLCK
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15387. .15531,15775. .15926,16131. .16229))
/gene="F7J8_30"
13626. .16229
                                                                                                                                   complement(join(8811. .8995,9120. .10082,10181. .10291,
10608. .10852,10996. .11147,11461. .11559))
/gene="F738_20"
8811. .11559
/gene="F738_20"
                                                                                                                                                                                                                                                         .10082,10181. .10291,
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                                                                                                                                                                                                                                                                                                                       /note="strong similarity to lacil0 laccase, Populus trichocarpa, EMBL:PTY13773"
                                                                                                                                                                                                                                                    complement(Join(8811. .8995,9120. .10082,10.
10608. .10852,10996. .11147,11461. .11559))
/gene="F7J8_20"
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/protein_id="CAB69833.1"
/db_xref="GI:6759428"
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/gene="F7J8_20"
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/gene="F7J8_20"
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/number=3
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                    8214. .8420
/gene="F7J8_10"
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COMMENT

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AACITSLSKNLLWFADISSSVAEDNKIDTLQLTEKKLEEHETNLRLNSSDNIAAVSSI
VLKKQRRSRARQGKRKCQDDQHIVDTFSEWEANDDLQVIGKLMEASDLKWNCWFPKNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental/protein_id="BAB09945.1"
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                                                           CDS
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ECRDIEDEQILCAIELSVSEIETIFSLGAKPKPREPEKVPLIDLRRAINTEIRLMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIRLPDMIAAAAMAMDESRLDDFDQIENLINLFPTKEDMKFLLTYTGDKGNCEQLFQYL
QEVVKVPRVESKLRVFSFKIQFGTQITKLTKGLNAVNSACEEIRTSQKLKDIMENILC
LGNILNQGTGRGRAVGFRLDSLLILSETRADNSKMTLMHYLCKVLASKASDLLDFHKD
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TQVATVMALYYPARGNAEALAHYFGYHYPFEQVTATLLSFIRLFKKAHEENVKQAELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MQQNSFFLGVNRDITDARTASGWSLCPVLDIDTTRYGVNVHVDD
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FEYSDMLEEVHEAQNRTLEEQSLQRMSLDSGRQSSKLQLDLNEPAKIEBHSDYYPNQFL
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VKREPERROGESSVSLAGKHGLDQPGGVVQELEACLISTGLIDKRYKSLMTRSRERNK
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HCKPQMKSSKGQKVVAKRSGRVKRKRSRRISLVAEGNYQQVSAAEAIVDISKKGRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(6389. .6616,6703. .7246,7345. .8423)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"/strain="Columbia"
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physically assigned Pl clones
DNA Res. 4 (3), 215-230 (1997)
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                                                       2 (bases 1 to 83599)
Nakamura, Y.
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                                                                                           Direct Submission
               DNA Res.
97471969
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                                                     REFERENCE
AUTHORS
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JOURNAL
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AAETNHASILKRYSTRYLDKKTGKAQVQTRYRGNQTSSTHDLCKHGKRREEDLVIKPWK
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LEKTDLEVKKVSRISENKSSKEDTIKNKEKAKIDEPVRCDDVLEKTSLDAQKVSRISE
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QQSSEKKIIRSTGKKSLSLLPSLPPPSEVVTGSDPRPIRQTTSRSKTSLPEKKQSGSA
NLVTNPKPESKIRPKRIGLKVTPPPPPTKQQMNFKKGKVLEPKPEDSTTTSIKFKIV
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GGRCFIADEMGLGKTLQAIAIAGCFISEGSILVVCPAVLRFTWAEELERWLPSCLPSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKGRDMRRFPGHKELWLYLKDFSEAFGLREMIRFNVRVEFVGEKEEEDDVKKWIVRS
SKSSPPKPVDAFTSSGEEKTGVDWGALRKRRGSRIPAADFKHMIINQVV°
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14411. .14544,14670. .14772,14856. .15043,15118. .15429,
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Arabidopsis thaliana
Rekaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
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Bevan, M., Van Der Schueren, J., Chuang, Y.J., Voet, M., Robben, J.,
Volckaert, G., Bancroft, I., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        32314 CTTATGATCATGAAATTCGTTGTAGCCTTGCCGCTAACAATGGAACAAATTGGATCCAC 32373
                                                                                                                                                                                                                                                                                                                                                                                                           TCAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGA 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1277 ACAATAGGTTTGATGGAATGGTGTTTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTG 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGAAAGATAAAGATTCC 1396
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Arabidopsis thaliana DNA chromosome 5, BAC clone F13G24 (ESSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATGGAAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTACACTTTATTATGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACAGTGACCG---CGG
                                                                                     3374 CATTGTCTTTGAGCTATCTTGGTAATTGTCTTTCTGCTGTAAAGTCCAAGACCGTTACAT
                                                                                                                                     CAGGTTTGTTACTAGCAAGCCCGATCGAGTTCGCTGGTGGTGGTACAACAAGCGATCG
                                                                                                                                                                                                                             TGAAGCATGACGCTAAGGCCATTGATGAAGAACAAGGAGTGGGAGAGCAACCCGAAGA
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EU Arabidopsis sequencing, project.
Direct Submission
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AL133421
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KEYWORDS
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SGNDPALVKTKINDFSYLSQVSKTFKDVNOTIQEHGPWASPRVGESGGAYNSGGRHVSD
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GWTPLHAAAKERKREAVKFLVGNGAFLPDDITDSRFNPPVQYCHGLEWAYEERKKLSE
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/product="anthranilate
hydroxycinnamoyl/benzoyltransferase-like protein"
/protein_id="pAB0949.1"
/db_xref="GI:10176719"
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                     /note="contains similarity to heparanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(31233. .31706,31923. .32819)
/note="gene_id:MXM12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.4%; Score 119.2; DB 1.9.2%; Pred. No. 1.3e-17;
                                          gene_1d:MXM12.7"
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complement(3628. 3850) // number=12 // complement(3851. 4026) // number=13 // number=13 // number=13 // number=14 // number=14 // number=14 // number=14 // number=14 // number=14 // number=15 // number=15 // number=15 // number=15 // number=16 // number=15 // number=16 // numbe	LEKTDLEVKKVSRISENKSSKEDTLKNKEKAKIDEPVRCDDVLEKTSLDAQKVSRISE NKNSKEERLKNIKNKEKTNIDEPVRPDDAVEKTLYVVESSVEKKKKHSTKSVKISET	OOSSEKK I IKSTCKKSLSLLPSLPPSEVYTGSDPRPIRQTISRSKTSLPEKKOSGSA NLVTNPRPESKI RPKRIGLKVPPPPPPTKQQMNFKKGKVLEPKPEDSTTTSIKFKIV VQEPKLRTSDVNKKSLKDKREGGKI NIGEGRREKVLRHRKVEVKKLQTLFNNVI FFTVNKI FFVDR GKYKAI VIK AGEBETVI GI OONUDFSOKK TIOSGSTSCAVVIECT	complement(57737458) //number=1	1145 11303 /gene="F13624.30"	/number=1 1114513478	/gene="fi3624.30" join(11145, .11302,1140011436,1153211715,1181411962, 1203712273,1237212561,1266512790,1290113000,	19093134/0. /gene="F13G24.30" /note="similarity to heparanase precursor, Homo sapiens,	ine proteases,	/product="putative protein" /protein_id="TAB62595.1" /db xref="R1:656299"	/translation="MAQBMKRASIVIQGARRVCETDENFVCATLDWWPHDKCNYDQCP" /translation="MAQBMKRASIVIQGARRVCETDENFVCATLDWWPHDKCNYDQCP" RQYSSYINMDLIFFYCHIFFKPIRFIGSSLQDQVIYDVGULFFYCFRPFQKMNSG FORESYOTHUR BARGING FOR THE AND AND THE FOREST FOR A RACK MIND IN MIND DE	LYAPIGETY EQQMYTKLLEISGPSVVDVVTHIYNLGSGNDPALVKKIMDPSYLSQVSK LVAPIGETY EQQMYTKLLEISGPSVVDVVTHIYNLGSGNDPALVKKIMDPSYLSQVSK	TEKDVNQTIQEHGPWASPWVGESGGAYNSGGRHVSDTFIDSFWYLDQLGMSARHNTKV YRRQTHVGGFYGLERGTFVPNPDYYSALLIMHRIMGKVANAVTDGPPPLRYAHCSK ODDAGTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTT	GRANG TELETINEONGERT VS VONGTINV ENABERRARGELLE LARKE SMIGSSKASUG YLINREET HITPENGVLRSKTMVLNGKSLK PTATGDI PSLEPVLRSVNSPLNVLPLSMS BIVID DANDA GAGET	11304 11399 11304 1200 1200 1200 1200 1200 1200 1200 12	/ 96126 - 12064 - 30 / number = 1 11/00 - 11/36	/genc11430 /genc11430 /gences	//UNINDEL1.2 1143711531 //CENES"F13624.30"	/number=2 1153211715
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gene exon CDS	intron	intron	exon	intron	exon	exon	intron	exon intron	exon	intron	intron	exon	intron	exon	intron	exon	intron	exon

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prediction programs including GRAIL (ftp://arthur.epm.orni.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, her) thtp://gnomic.staniford.edu/GENSCANW.html), and NetplantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; editoctyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicacee; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-MRR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Dec 17, 1999 this sequence version replaced gi.2088638. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                              17149 TTTTCCATTTAGAAAAACTTTTGGGAGCGATGGTGGTTCACATTGGAAGCTCTCCGAGGT 17208
                                                                                          17209 TTAAGATGTATGAATGCGAGTTTGGGATGGGAAAAGCGGTTGCGGTTAGAAGCGGGTTATG 17268
                                                                                                                                                                                                                                                             1397 TCATGGAAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTACACTTTATTATGAGC 1456
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AF002109.2 GI:6598791
                                                                                                                                                                                                                                  ATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGAGGGTTGGAGAAGAAGAGTTCC
                                              TCAAGGTTTACGACGTGGATTTTTGGATGGGGAAAGCCAGAGAGTGTGAGGAGTGGTTCGA
                                                                                                                                        1277 ACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              743 ACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16849 CTTCTTTTCAAGCGTTAGCCGCATTTATGTGGAGATGCATTACAAGAGCAAGAACTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      923 AGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAAGCATGACGCTAAGGCCATTGATGAAGAAACAAGGAGTGGGAGGAGCAACCCGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTTCAGT - - - ACAAAGATGCTGGAGTGAACTGTGGTTGCTTGGAAGTTCGCCAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      683 GAGTCAAGCTCAACCTCTCTCAACCATCAGATGCACCCGAACATGCTAAGTCAGCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803 AGTTAGCAATTGACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGAGGCGCCATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 88095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 119.2; DB 13;
larity 49.2%; Pred. No. 1.3e-17;
Conservative 0; Mismatches 463;
                                                                                                                                                         /number=4
11963. .12036
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/gene="F13G24.30"
                                                                                                             11814. .11962
/gene="F13G24.30"
                                                                                                                                                                                                                                                     12037. .12273
/gene="F13G24.30"
                                                                                                                                                                                                                                                                                                                            12274. .12371
/gene="F13G24.30"
                                                                                                                                                                                                                                                                                                                                                                                                12372. .12561
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/gene="F13G24.30'
                                         11716. .11813
/gene="F13G24.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=6
12562. .12
                        /number=3
11716. .11
                                                                                            /number=3
                                                                                                                                                                                                                                                                                                           /number=5
                                                                                                                                                                                                                                                                                                                                                                             /number=5
                                                                                                                                                                                                                                  /number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Sim
Matches 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                              intron
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22753. .22816
/rpt_family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAKNNKLNAMQKLWHWLNYVFFSLMSVAAAIAAVRLIAVDSKNFHVFADL"
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29872. .29961,30172. .>30411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(29280. .29414,29559. .29658,29750. .29787,29872. .29961,
30172. .30411)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRPVARMGAFSVCKPGYMAPCEGPLVQASRPDSLAGKFLQSLCYDPIIPSKCGHGCCN
HQDSTTLSSSSVLGSEFVDYEEHSSAELDKELISISNDLNNTAWIRSGKEAEQSLKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGLICAIFAIGIPHLSALGVWLGVSTFLSLIYIVVAIVLSVRDGVKTPSRDYEIQGSS
KLFFITGAANLVFAFROMLPEZOATVRQPVKRMWARAFYGFFAGVLPWAYTF
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GNPFAIKNLLFRIMARGGYIAVSTLISALLPFLGDFMSLTGAVSTFPLTFILANHMYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGINSAYVLGYSGTIMVPLGWIGGVVGLLIATAISLYANTLIAKLHEFGGRRHIRYRD
LAGFIYGRRAYHLTWGLQYVNLFMINCGFIILAGSALKAVYVLFRDDHTMKLPHFIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSNTEIVYQLYPSMVRRISNASPKEHLPQEEETGVLSDDKMDDEAKEPPREQNSKTGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative MYB family transcription factor"
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conplement(20519. 20562)
/rpt_family="(TA)n"
22037. 22139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="proline transporter 1"
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/db_xref="G1:2088642"
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                                                                                                                      /note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="At2g39880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28838. .>30411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="T28M21.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="T28M21.6
                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .28451
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//rpt_family="POLY_A"
//rpt_family="POLY_A"
join(<770. .853.968. .1059,1190. .1278,1443. .1674,1811. .2363,
2453. .2556,2790. .3035,3146. .3272,3336. .3579,3664. .>4244)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <770. .>4244
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/note="T517.15"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="(GAAAA)n"
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13781. >15094
                                                                                                                                                                                                                                                           We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bloinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLQTTRSWDFMNLTLKAERNPENESDLVVAVIDSGIWPYSELFGSDSPPPPGWENKCE
NITCNNKIVGARSYYPKKEKYKWVEEKSVIDVTGHGTHVASIVAGRKVEKAGYFGLAE
GTMRGGVPNAKIAVYKTCWRVIRKNGREDSVCREDNILKAIDDAIADKVDIISYSQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFETKLELEGEBÜRP ITVYDT UTFFETQDSFYPLLUBKAPPESTRKRELTAERNGYSIL
SNYDEKDKGKDVFFEFAQINLLDEAIKEREKGAIVLGGKSYDFNESIKLQFPIASIFL
DEQKKGKLMDYYKKDQSKERLAKIHKTEEIPREEGWVPTVAHLSSRGPNCDSFLANIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MAIAFHTFLLQLLLFFRASFAEANDSRKTYLVQMKVGGHRYGSS
SGHQELLGEVLDDDSYKESFTGFSASLTPRERQKLMSKTTTVSSRRREENSKRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFTPLQKDKVSWAFLRALKNGILTSAAAGNYANNGKFYYTVANGAPWVMTVAASLKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNSHMNNCFQPDIAAPGLDIIAGWPENVKLSSDRPANDYRHLRFNIMSGTSMACPHAT
GLALYLKSFKRWSPSAIKSALMTTSSEMTDDDNEFAYGSGHLNATKVRDPGLVYETHY
QDYIDYLCKLGYNTEKLRSHVGSDKIDCSKTEIDHDADLNYPTMTARVPLPLDTPFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFHRTVTNVNDGEFTYLREINYRGDKDFDEIIVDPPQLKFSELGETKTFTVTVTGISK
RNWNKNRAFMTRNTWLTWTEKDGSRQVRSPIVIYSIKGPKACM"
Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by LRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative serine protease"
/protein_id="AAB95271.2"
/db_xref="G1:6598792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .9962, aa: Ala)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at@tigr.org
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//note="Sequence from clone T28M21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Sequence from clone T517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(11732. .11793)
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/gene="At2939860"
/note="T28M21.2"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/chromosome="II"
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/anticodon=(pos:9960.
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                                                    /translation="MSFTGTQQKCRACEKTVYPVELLSADGISYHKACFKCSHCKSRL
QLSNYSSMEGVVYCRPHFEQLFKESGSFSKNFQSPAKPLTDKPTPELNRTPSRLAGMF
SGTQDKCATCTKTVYPIEKVTVESQCYHKSCFKCSHGGCPISPSNYAALEGILYCKHH
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Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-AUG-2000) Takuji Sasaki, National Institute of Aproblological Resources, Rice Genome Research Program: Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
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Oryza sativa genomic DNA, chromosome 6, BAC clone:OSJNBa0075G19,
                                                                                                                                                                                                                                                                                                                                                                                                                                            1040 CAGGTTTGTTACTAGCAAGCCCGATCGAGTTGGTGGTGATACAACAAGCGATCG 1099
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                                                                                                                                                                                                           860 TCTCCACATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGTCACACGTGCGCGCCCAAC 919
                                                                                                                                                                         Gaps
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                                                                                                                                DB 12; Length 110531;
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:OSJNBa0075G19
                                                                                                                                                                         Indels
LIM-domain protein"
                                                                                                                                                  Pred. No. 1.7e-14;
0; Mismatches 268;
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                                                                                                                                Score 106.2;
              /protein_id="AAB95275.1"
/db_xref="G1:2088643"
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                                                                                                                                Query Match 6.6%;
Best Local Similarity 49.9%;
Matches 267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Score 102.8; DB 13; Length 88318;
Pred. No. 1e-13;
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Tel:81-298-38-7441, Fax:81-298-38-7468)
The orientation of the sequence is from clone.
                                                                                                                                                                                                                                               /clone="OSJNBa0075G19"
19394 c 19436 g 24509
                                                                                                                                     /organism="Oryza sativa
                                                                                                                                                                 /cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                      Location/Qualifiers
                                                                                                                                                                                                                      /chromosome="6"
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Best Local Similarity 46.1%;
Matches 455; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNRS, Avenue de la terrasse, 91198 Gif sur Yvette Cedex, FRANCE (Cation/Qualifiers
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales, Fabaceae, Papillonoideae, Medicago.
              AAGCCAGAGAGTGTGAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTGTATTTGTAC 1308
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Submitted (28-MAR-2001) Ratet P.
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/note="Sy5 (RB) locus"
                                                                                                                             1369 GAGAGGTTGGAGAAGATAAAGAGTT 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(2238. .2668,2807. .3330,3449. .4119))
/note="similarity to various predicted genes, Arabidopsis thaliana and Oryza sativa"
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On Apr 20, 2000 this sequence version replaced gi:6434207.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
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Bargues,M., Collado,M.C., Navarro,P., Terol,J., Perez-Alonso,M.,
Mewes,H.W., Rudd,S., Lemcke,K., Mayer,K.F.X., Quetier,F. and
1259 GTGTGAGGAGTGGTTCGAACAATAGGTTTGATGAAGGAATGGTGTATTTGTACCAAGGCAAAA 1318
                                                       Choisne, N., Robert, C., Brottler, P., Wincker, P., Cattolico, L., Artiguenave, F., Saurin, W., Weissenbach, J., Mewes, H.W., Rudd, S. Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATF11C1 111122 bp DNA PLN 19-APR-2000 Arabidopsis thaliana DNA chromosome 3, BAC clone F11C1.
                                                                                                                                                                                                                                    ATGGAGGAAGAAGCATTGATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGGTTGG
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/variety="Columbia"
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166494 7218 bp Sequence 14 from patent 166494 166494.1 GI:2724471

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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1530-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Kisarazu, Chiba 292-0818, 1438-52-934)
Address for correspondence: koos@kazusa.or.jp
Por the latest information on annotation of this clone, please see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sixty
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Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21H1
AB020742 BA000015
AB020742.1 GI:3985931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1164 TCAGTACAAAGAFGCTGGAGTGAACTGTFGTTGCTGGAAGTTCGCCAAGGTTCAAGGT
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                                                                                                                                                                                                                                                                                                                                                            Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1344 GATTAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGAAAGATAAAGAG 1392
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                                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%; Score 67; DB 10; Length 72 Best Local Similarity 2.0%; Pred. No. 2.5e-05; Matches 7; Conservative 221; Mismatches 121; Indels
                                                   1 (bases 1 to 7218)
Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                                                                                                                    1929
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                        /organism="unknown"
                                                                                                                                                                                                                                                  1491 c 1486 g
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DNA Res. 7 (1), 31-63 (2000)
20181125
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Arabidopsis thaliana
                         Unclassified.
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Unknown
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JOURNAL
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CDS
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                                                                                                                                                                                                                                                                                                 CDS
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi7c-K2lH1
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein.'
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), NetGene2 (5.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/netGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gramlin.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is KBAID and the 3' clone is KBGI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mitsui TAC"
complement(join(683. ,778,1044. ,1247,1325. ,1959,2053. ,2283,
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//db_xref="61:1017759;
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MDTASMLDEATHYVRELKQVQSLEEQAVVTGGGGGGGGRVLIGGGGMTAASGGGGGG
GVVMKGCGTYGTHQMVGNAQILR"
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HSDEFDIIDGEESFEVTEEDDGVTDRRSLYWRRTKYYISYGALSANRVPCPPRSGRSY
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DWCSDFDITWFELPNIGNIHGGFMKALGLQNNCSWPKEPLSNPDRKSPLAYYSIRDSL
KTLIAQNKNTKFVLTGHSLGGALAILFTAVLVIHHETELLERIQGVYTYGQPRVGDSK
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VWPQRTSENYQSFIGHLDTRVSLDWTLNREDGEKYYAALSIMASKIAYENAARIKHVV
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QSDENFFLLRGIIKMMASAILEFIRSFTIVAEKGSEYSEGWLLKGGRALGIIVPGVSN
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7772. .8497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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/note="emb|CAB62312.1
gene_id:K21H1.2
similar to unknown protein"
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/note="gb|AAF64534.1
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/evidence*not_experimental
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FFSPKFIGLISFTSGFRPVSNYGAGIVLGIDTGIWPDSPSFHDDGVGSVPSKKGACE
FNSSSLCNKKLIGAKVFNKGLFANNPDLRETKIGQYSSPYDTIGHGTHVAAIAAGNHV
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LSFEDDDDNOFGLENDPIAVASPALQKGVFVVTSGGNDGPYWSLINGAPWIWTVG
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FSEKNEKLSYTVKLESPRGLQENVVYGLVSWVDEDEAEFEVSCSVVATSLVQES
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MKTIVURGNUI SEIVSASULCFHINKIDVPHAPAPERKRSGILSHFYVRNPEGTGYP
IGWKEVSDENSKNGCNVLSIENSERALLANLLELLELINKLDSDILVGHNI SGFDLDVLL
QRAQACKVQESHWSK TGRLKREFMPKLKGNSNYGSGAPPGLMSCIAGRLLCDPDLCSR
DLLKEVSYSITDLSKTQLNRPRKEIAPNDI RKWFQSSKTLVELIECGETDAMLSMELM
FHLSVLLLFTLQLTNISONLWGKTLQGRAQATERYK LLIPSKREILDRD ISOKKEI
KSSKRRMDY AFBDRNYDELDALLTENDPSKGSKTKKGPAYAGGLVLEPRKELYDKYV
LLLDFNSLYFSIIQEYNICFTTIPRSEDGVPRLPSSQTPGILPKLMEHLVSIRKSVKL
                                                                                ASLANEKSVĮJDNLGDDCNEIVRCFGEDRTVENGEEMHNLFLEYASRGSLESYLKKLAG
EGYPESTYRRHTGSVLRGLRHIHANGFAHCDIKLGNILLFGDGAVKIADFGLAKRIGD
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VLVKEEDFVVNMKTEDVSTSPRCPFEFPDWVSVSSGSQTIDSPDERVASLVTDMIPDM
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SKKYKETDFAQYDGILLBAQYDPDSBDRKHTRRLLGGTVPYTIFKKLESYAS
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RKTEVKSELGVKEVFTLNATIDMKEKDSALSATAGWKEAMGKVGTENGALLGSSSEGK
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IPNDSIFPSHELIMLEQEVKDSRLSPESFRGKLHEMASKLKNEIAQELLQLNVSNFSM
APVKRNYAFERPDVPAGEQYVLKINYSFKDRPLPEDLKGESFSALLGSHTSALEHFIL
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VDLVQNHLNLEVIYGDTDSIMIHSGLDDIEEVKAIKSKVIQEVNKKYRCLKIDCDGIY
KRMLLLRKKKYAAVKLQFKDGKPCEDIERKGVDMVRRDWSLLSKEIGDLCLSKILYGG
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LAQQIHPVVSRLCAEIQGTSPERLAECLGLDPSKYRSKSNDATSSDPSTSLLFATSDE
ESKKPATPETEESDSTFWLKLHCPKCQQEDSTGIISPAMIANQVKRQIDGFVSMYYKG
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ranslation="MEWIRGETIGYGTFSTVSLATRSNNDSGEFPPLMAVKSADSYGA
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complement(join(26828. .27019,27114. .27179,27258. .27323.
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20278. .20342,20515. .20665,20698. .20883,2116. .21279,
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gene_id:K7!":
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/note="gene_id:K21H1.5"
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ORIGIN
AP003279/c
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                                                                               ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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RSDDETKRCVICQQKLKDNEEVSKLGCGHDFHFGCIKNWLMVTNKCPLCNREVV"
join(33235. .33402,33654. .33791,33873. .33971,34064. .34367,
                     /evidence=not_experimental
/protein_id="BAB10945.1"
/db_xref="GI:1017599"
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                                                                                                                                                                                                                                                                              /evidence-not_experimental
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/db_xref="GI:1017559"
/translation="MDPNEDNSEIPDSPFSFWWLLFGDDWDLWDTYSPVDADDISPDP
                                                                                              SSAETFFPSVSGGAVSSVGYGVSETGQDKYAFEHKRSGAKQRNSLKRNIDAQFHNLSE
KKRRSKINEKMKALQKLIPNSNKTDKASMLDEAIEYLKQLQLQVQTLAVMNGLGLNPM
                                                                                                                                                                                                                                                                                                                                                                TLDVNGDGPAIEPGSLLRTISWETTFEQDSLQSWNDEQSETTSVVEYTDVSSHGNTFT
NEEETLERYWRNWLQSSTNEQSETGSQEEYTNASSHGGTFIYEEETLEQYWRNWLQSS
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                                                                                                                                      RLPQVPPPTHTRINETLEQDLNLETLLAAPHSLEPAKTSQGMCFSTATLL"
complement (101n(29326. 29986, 29960. 30082,30390. 30512,
30845. 30958,31036. 31233))
/note="gene_id:K21H1.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               34837. 35225)
/note="contains similarity to MAP3K-like protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37972 AAAGCGAAAGCTAACGGCGAGGTTGACTCCGATGATGGGAAAATATCGTCGCTTCAAGCG 37913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 305; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 12;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                         similar to unknown protein"
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Best Local Similarity
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RESULT

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Assaki,T., Matsumoto,R.

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Submitted (19-FBB-2001) Takuji Sasaki, National Institute of

Agrobiological Resources, Rice Genome Research Program; Kannondal

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasakidebr-affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given however the sizes of the gaps between them

are based on estimates that have provided by the submitter. This

sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.

* NoTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* the accession number will be preserved.
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                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19433 GTCTGGCGCCCGACGCGACGAGCACGTTCCGCATGGCGGTGAACTGCCGGCACAGGCTGC 19374
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*** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                        1 (sites)
Saski, ". Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0529E05
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0; Mismatches 282;
                               Oryza sativa chromosome 1 clone P0529E05, PROGRESS ***, in ordered pieces.
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                                                                                                                                    GI:13027309
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137205 bp
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Matches 256; Conservative
                                                                                                                                                                       HTG; HTGS_PHASE2
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918 -ACTCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGGAAAAGGGTTG 976
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Cryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:181096Al0

L bublished Only in DataBase (2001) In press

E (bases 1 to 151703)

Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

Alforbiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mall:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

* This sequence will be replaced as soon as it is available and

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* That a continuality be repeatived.
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                   19073 GCGCCAACAAGTTCGATGGCAAGATGTCGGCGTTCCCTGCCCGCGCGGGGACGGCAGCG 19014
                                                                                                                                                                                                                         19013 TGGACATCGAGGTGTGCCTCGCCCCGACACCATGGCGGCGCTGCTCCGCGACAGCGAGT 18954
                                                                                                  1274 CGAACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCA 1333
                                                                                                                                                                                   1334 TTGATGTGGAGATTAGTTTGGAAGCAAATGCTATGGAGGTTGGAGAAAGATAAAGAGT 1393
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Oryza sativa (cultivar:Nipponbare) DNA, clone:B1096A10.
Oryza sativa
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3b_est90:*
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90-9887 90-9887 90-9881 90-98811 90-98812 90-98814 90-98816 90-98816

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_inv4:* em_gss_rod6:* em_gss_rod7:*

gb_gss28:* gb_gss29:* gb_gss30:*

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em_gss_rod8:* gb_gss35:* gb_gss36:* gb_gss37:*

, Fraser, C.M., Martin, G.B., Tanksley, S.D. and Glovannoni, J. Generation of ESTs from tomato fruit tissue Unpublished (1999). VNAL Unpublished (1999). Contact: David Frisch Classic Contact: David Frisch Classon University Genomics Institute		<pre>source 1583 /organism="Lycopersicon esculentum" /cultivar="TA496" /db_xref="taxon:4081" /clone="cirr3F37" /clone=lib="tomato fruit mature green, TAMU" /risuna frune="fruit nationary"</pre>	/dev_stage="mature green (3.5 days pre-ripening)" /lab_host="SoLR" /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Si Xhol; cLE: - Fruit were tagged at the lom stage and harvested 3-5 days prior to ripening. Fruit were co half to verify the seeds were indeed 'immature' an seeds and locules were discarded prior to freezing	pericarp" 142 a 140 c 117 g 184 t	Query Match 9.4%; Score 152; DB 113; Length 583; Best Local Similarity 56.4%; Pred. No. 1.3e-27; Matches 325; Conservative 0; Mismatches 245; Indels 6; Gaps	58 CAAAGTICTTGAGAAATGCOGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGT 13	118 CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 17 1 1 1 1 1 1 1 1 1	178 CTACAGATTCCGCCATCCTT3TCCCAACTCTAAATTTATCATTCATCCATTAAATC 2:	235 GICCCTTTCCCTTGTTCTCAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGT 29 1	295 AGATTCCTCCGATAGAATGCCGGTTACAAGAAGGGGACTCCGTTTCTTAAC 3:	355 AATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTA 4)			
TITLE JOURNAL COMMENT	FEATURES			BASE COUNT ORIGIN	Query Best Match	Qy	Oy Dp	Qy	Oy Db	Ογ Db	o a o	op Oy	qa "o	S 8 8
Description	AW221050 EST297519 BG599447 EST504342 AW221049 EST297518 BE922784 EST426553 BG591758 EST499600 BE434257 EST405335	AW016206 EST307245 AW030034 EST356777 BF096979 EST400516 AW650280 EST328734 BE921494 EST425179 BG598154 EST4456832 BG097054 EST446832	BE922746 EST426515 BE053202 EST438432 BE187619 EST336180 AW102336 S486406.y BE220468 EST44237 AI490445 EST24871 BG584708 EST446469	BEA33920 EST404998 BF051101 EST436276 BEA36185 EST407263 BE922378 EST426147	BE92357 EST427341 BE922950 EST426719 BE921952 EST425721 BE921953 EST445722 ME31951	AM016119 ES1290694 BGG97680 EST462199 AW776512 EST335577 BG444830 NF070A05E	BF639071 NEVIALZE BF639071 NEVIALZE AW560686 EST315734 BF384678 EST486439 BF071604 SF34575757	BF278256 GA_ED003 AL386584 MtBC35E10 BF643475 NF0044105E BF6643475 A-CR	EST35 EST42 330 C		EST 07-DEC-1999 TAMI INCODERSION ESTIME		Streptophyta; Embryophyta; Tracheophyta;	;; Solanaceae; Solanum; Matern,A.L., Holt,I.E., Liang,F., Bowman,C.L., Ahn,S., Ronning,C.M.
SUMMARIES Query core Match Length DB ID	9.4 583 113 9.3 690 155 9.3 690 155 8.7 763 142 8.2 591 167	7.9 48/ 118 7.7 487 128 7.6 482 144 7.3 518 119 7.1 564 142 7.1 659 155	108.8 6.7 574 142 BE922746 103.6 6.4 403 143 BF053202 89.4 5.5 687 111 AW10236 85.8 5.3 575 142 BE920468 77.8 4.8 783 155 BG584708	4.6 451 167 4.6 578 143 4.6 542 167 4.5 411 142	4.5 456 142 4.5 354 142 4.4 414 142 4.2 368 142	4.0 386 173 4.0 686 120 3.8 642 153	3.8 681 151 3.6 694 115 3.6 829 155 3.6 411 145	3.6 658 146 3.6 526 105 3.6 649 151 3.5 708 138	3.5 311 166 3.4 307 142 3.4 489 138 3.3 648 154		AW221050 583 bp mRNA EST297519 tomato fruit mature green.	e cLEF3F3, mR8	tomato. Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophy Snormatonbuta: Mannolionbuta: endioc	Asteriade: eusterids I; Solanales; Lycopersicon. 1 (bases 1 to 583) Alcala,J., Vrebalov,J., White,R., Ma Opton,J., Hansen,T., Craven,M.B., Bo
Result No. So			14 10 15 10 16 9 17 17 18 8 19 7			330 330					RESULT 1 AW221050 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS

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ript SK(-); Site_1: EcoR1; Site_2: e tagged at the lcm stage and or to ripening. Fruit were cut in ds were indeed 'immature' and the discarded prior to freezing the STTAGCCGGAATTGATTTGGCCGGT 294 CGCCGGAGATCACAGAGGGATTCTTA 414 ACCGATTGTAACCTCCGGCGACGAAGT 474 AAATTTATCATTTCATCCATTAAATC 234 ITTTCTGCATTTTAATAAATTATGGGT 594 ACCEGACECCETCECCGAGTTTACAGT 117 STCTGATGCAGAACACCATCTGCATTT 177 STITCGCCGIATGAGGCGGGATATTATI 128 STCCAACACGGTATATGCATTGGACG 534 6; Gaps en (3-5 days pre-ripening)" ; DB 113; Length 583; 1.3e-27; ches 245; Indels 6; it mature green, TAMU" ricarp" GTT 630 184 t

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TTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTT 486
                                                        359 CTTTGTTCCTACGTTAGGGGAACCTAAGGATGCACCCGGGGTCCAATTAGCTCCGGTCTT 418
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                                                                                                                                                                                                                        SM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; endicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 690)

S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,

Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.

Generations of Esrs from sprouting potato eyes

L (Dnpublished (2000)

Ton fact (2000)

The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries

Dlysshor tell 1-800-711-6195, email cdna@tesgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-weetor: paluescript SK(-); Site_1: EcoRI; Site_2: Xhof: Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers: The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                             BG599447 690 bp mRNA EST 12-APR-2001
EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' seguence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CATITCCAAACCGGATITGTTGTTATTCCTCTTAAAAATTCACTCTCCTT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 TAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 151.4; DB 155; Length 690; 77.1%; Pred. No. 1.9e-27; ve 0; Mismatches 231; Indels 6;
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/clone="csTs25122"
546 TCTACTCCACAAATTACGTGGACATGAACCAATCTT 581
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Best Local Similarity 57.1%;
Matches 316; Conservative
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                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                              potato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                             LOCUS
                                                                                                                                                                                                                              ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                       KEYWORDS
SOURCE
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l (bases I to 606)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Opton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Compublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                   AW221049 606 bp mRNA EST 07-DEC-1999 EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum con clore cLEF3F1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seeds and locules were discarded prior to freezing the pericarp"
TGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCA 546
                               547 AGTICITGGIGATGCCAGTICITTTCTGCATTTTAATAAATTATGGGTTTTGGTTGACAA 606
                                                                                                                                                                    479 TGTTGTTGGTGGTGGAGCTACCATAGTAGGGTTCATTAGGGCGTGGGCTCTACTCCATAA 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
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/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db xref="taxon:4081"
/clone="cLEF3F1"
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Pred. No. 2.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4293 Email: dfrisch@CLEMSON.EDU
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Best Local Similarity 56.6'
Matches 320; Conservative
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Unpublished (2000)
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Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE922784 570 bp mRNA EST 02-OCT-2000
EST426553 potato leaves and petioles Solanum tuberosum cDNA clone
CSTB22E2 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnafresgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                425
                                                                                          129 TTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAA 188
                                                                                                                                                                                                               249 AGATACAAACG---GATATCCTGAGTTACGTTATGTGACAGGAGATTCTGTGTCTGTTAC 305
                                                                                                                                                                                                                                                               414
                                                                                                                                                                                                                                                                                                                                 474
                                                                                                                                                                                                                                                                                                                                                                                                                               426 AGCCCCCCTTTAGCCATTCAGGTGACACTTTTTCCGAATCTTGGTGTATCCATTGGTTT 485
118 CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                                                                                                                                                                                                                                                                                                                                                                                                475 ATTACCACTTTTGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATCTTCATCAAGTTCTTGGTGATGCCAGTTCTTTTTCTGCATTTTAATAAATTATGGGT 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACAGATTCCGCCATCCTTGTCCCAACTC - - TAAATTTATCATTCATCCATTAAATC
                             69 CCCTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGGATATTATT
                                                                                                                               235 GTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGT
                                                                                                                                                             189 ITCACTCCCCCCCCCCCCCCAAACACTATACGCCCCTTAGCCGGAAACGTTGCTTGTCCACT
                                                                                                                                                                                            295 AGATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAAC
                                                                                                                                                                                                                                                              355 AATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SolR"
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/organism="Solanum tuberosum"
/cultivar="Kennebec"
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/clone="cSTB22E2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    546 TCTACTCCACAAATTCGGTGGACAT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 TTTGGTTGACAAATCCAATGGAGAT 619
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KEYWORDS
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EST 499600 P. infestins-challenged leaf Solanum tuberosum cDNA clone BPLI10A14 5' sequence, mRNA sequence.
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1 (bases 1 to 763)
Zhang, P., Hernandez.M., Tornqvist, C.-E, Wirtz, U., Loukolanov, A., Rangel, P., Haberlach, G.T., Cho, J., Chlemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Helgeson, J., and Baker, B.
Generation of ESTS from Potato Leaves Challenged with Phytophthora incompatible Reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 CGTTTTTCGACATGCGATGGTT3ATCTCTGATGCAGAACACCATCTGCATTTCTACAGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGGATATTATTCTACAAGC 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 ATCACTTTGTTCCTACGTTAGGGGAACCTAAGGATGCACCCGGGGTCCAATTAGCTCCGG 453
          greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                          157 TCCCCATTTCCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAATTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAG
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The Institute for Ganomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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Leaflets and petioles were isolated from 8 week
                                                                                                                                                                                                                                                                 Length 570;
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Best Local Similarity 57.0%; Pred. No. 9.2e-26;
Matches 305; Conservative 0; Mismatches 224; Indels
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                                                                                                                                                                  /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Rennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 CTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGGTAGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 TTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTT 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 GACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTCGGCCAT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTACAAGCTCCCCATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 CCTTGTCCCAA---CTCTAAATTTATCATTCATCCATTAAATCGTCCCTTTCCCTTGTT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TCCAAACCCGATTTCGTTCAAAACATTATTCCTACTCTTAAAAATTCACTCTCCCTCACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 ATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGC 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 140.6; DB 155; Length 763;
Pred. No. 9.8e-25;
0; Mismatches 259; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="kennebec"
/db_xref="taxon:4113"
/clone="BbLi10A14"
/clone="lb="P. Infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
                                               /organism="Solanum tuberosum"
             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              156 g
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.3%;
Matches 346; Conservative (
Seq primer: M13F-R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 GTAAAGGACCCATAT 610
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ORIGIN
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Anote—"Vector: pBluescriptSkmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
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                                                                                                                                                                           Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                            l (bases 1 to 591)
Jaclas, Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                     EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 GTTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 CAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCT 387
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24-JUL-2000
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Pred. No. 6e-23;
0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="cLEG15H6"
/clone_lib="tonato breaker fruit, TIGR"
/tissuc_type="pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
Clemson University
                                           clone cLEG15H6, mRNA sequence.
BE434257
BE434257.1 GI:9432100
  mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: dfrisch@CLEMSON.EDU
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56.6%;
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Contact: David Frisch
591 bp
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Location/Qualifiers
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VERSION
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AUTHORS
     61
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AW930934
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tankaley, S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon hirsutum
Sukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                    EST307245 L, hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
AW616206
AW616206.1 GI:7322240
                                                                 627
                                                                                              414 TATAGCAGGGTTCATTAAGGCGTGGGCTCTACTCCACAAATTCGGTGGACAT---GAACA 470
                                                                                                                                                 628 GTTCCTTCCACTTTCTTCTTACCTATGTACGACAGATCTGTGGTGCAAGATCCATTTCA 687
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DB 118; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.9%; Score 128.6; DB 118; Lengt
Best Local Similarity 57.2%; Pred. No. 9.4e-22;
Matches 274; Conservative 0; Mismatches 199; Indels
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Corganism="Lycopersicon hirsutum"
/db_xref="taxon:62890"
/clone="cLHT1D15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
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                                                                                                                                                                                               688 TATTCGTCGAAAATCTACAATGAAAGAAA 718
                                                                                                                                                                                                                             531 ACAAGGGATGTCCATCTGGGAAGAAATGAAA 561
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Email: dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AW616206
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'Yourcalain', Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Glovannoni, J. Generation of ESTs from tomato fruit tissue (Generation of ESTs from tomato fruit tissue contact: David Frisch (1999)

Contact: David Frisch (Clemson University Genomics Institute (Clemson University Genomics Institute (Clemson University Genomics SC 29634, USA)

Tel: 864 656 4366

Fax: 864 656 4293

Email: dfision@clemson.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eŭkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW930934 497 bp mRNA EST 30-MAY-2000 EST356777 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF42M23 5', mRNA sequence.
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121 TITCGTICAAAACATTATTCCTCCTCTTAAAAATTCACTTTCCCTCACTCTCAAACATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                               382 TTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCT 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 TTATCTCATTGGCGACCATCCGCGTAATGCTAAGGATTTTTATCACTTTGTTCCTAAGTT 357
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                                                                                                                                                                                                                                                                                                                                                                                                     GCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 GCCAGAACCGATTGTAACCTCCGCGACGAAGTATTACCACTTTTGCTTTACAGGTGAC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 GGTGTTCTCCAACACGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CICTAAATTTATCATTTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTT
                                                                                                                                                                                                                                                                                                                                181 TATGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACG---GATATCCTGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="tomato fruit mature green, TAMU"
fitssue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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Lycopersicon.
1 (bases 1 to
                                                                                                                                                                                                        Similarity
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DEFINITION
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KEYWORDS
SOURCE
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van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L.,
Nlerman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Giovannoni, J.J.
Generation of ESTs from tomato nutrient-deficient roots
Contact: David Frisch
                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
                                                                                                                                                                                                                                             475
                                                                                                                                                                                                                                                                                                                                                                                                 655
                                                                                                                                                        356 ATTGCAGAATCGAGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTAT 415
                                                                                                                                                                                                            236 TCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTA 295
                                                                                                                                          GATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACA 355
                                                              Gaps
                                                                                                                 61
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                                                                                                     AAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTA
                                                                                                                                                                                                                                                                                               476 TTACCACTTTTGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGC
                                                                                                                                                                                                                                                                                                                       239 GCCCCGCTCTTAGCCATTCAGGTGACACTTTTTCCGAATCTTGGTGTATCCATTGGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                 359 CTACTCCACAAATTCGGTGGACAT---GAACAATTCTTATCGAATGAGCTAATTCCATTT
                                                                                                                                                                                                                                                                                                                                                9
                                    Length 497;
                                    Score 125.2; DB 122; Lengt
Pred. No. 6.7e-21;
0; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA clone CLEW18020 5' sequence, mRNA sequênce.
BF096979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST400516 tomato nutrient deficient roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                    656 TACGACAGATCTGTGGTGCAAGATCCATTT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar-"TA492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF096979.1 GI:10902689
                                    7.7%;
58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 bp
                                                              Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon.
                                                  Local Similarity
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                                      Query Match
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COMMENT
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/note="Vector: pBluescriptSKmcUadapt; Site_1: 5' EcoRI; Site_2: 3' XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TTTTCAAACCCGATTTCGTTCAAAAATTTCTCTCCTCTTAAAAATTCACTCTCCTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 GAATGCCGGAGTTGCGTTACAAGAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 AATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTGTCGTTTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTCCGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TTGACCATGTTTGGTTTAGGGTTTTCGCCGTATGAGGCGGATATTATTTTACAAGCTCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 ccarrcaggraacacrrrrrccaarcrrggrarccarrggrrrcacraaccarcarg 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 ATCCTTGTCCCAA---CTCTAAATTTATCATTCATCCATTAAATCGTCCCTTTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 GCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST328734 tomato germinating seedlings, TAMU Lycopersicon esculentum cDNA clone cLEI12F13 5', mRNA sequence. AW650280 GI:7411518
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                          Length 482;
/clone="cLEW18020"
/clone_lib="tomato nutrient deficient roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Score 124; DB 144;
Pred. No. 1.3e-20;
0; Mismatches 205;
                                               /tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                          7.68;
56.48;
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Matches 307; Conservative
                                                                                                                                                                                                 Unpublished (2000)
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                                                                                                                                                                     TITLE
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                                                                              REFERENCE
                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                          COMMENT
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                                                                                                                                                                                                                                                                                                                                     /crganism="Lycopersicon esculentum"
/cultivar="TA496"
/cultivar="TA496"
/dutivar="TA496"
/clone="Laxon:4081"
/clone="cLE112F13"
/clone="cLE112F13"
/clone="taxon:4081"
Nierman, W., Fraser, C.M., Giovannoni, J.J., Martin, G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potato leaves and petioles Solanum tuberosum cDNA clone 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 CTTAGCCGGAAACGTTGCCTTGTCCACTAGATACAAACG---GATATCCTGAGTTACTTTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 CGCCGGAGATCATCAGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 ACCGATTGTAACCTCCGGCGACGAGTATTACCACTTTTTGCTTTACAGGTGACGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 CTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATGCCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 TCCGAATCTTGGTGTATCCATTGATTTCACTAACCATCATGTTGTTGGTGATGGAGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 119; Length 518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173; Indels
                                                  Generation of ESTs from germinating tomato seed
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ilarity 57.3%; Pred. No. 2.2e-19;
Conservative 0; Mismatches 173
                                                                                                                                           Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                            Clemson University Genomics Institute
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                                                                                           Contact: David Frisch
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Solanum tuberosum
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hes 236;
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and effectilized freely. The tissue was immediately frozen in final attractor.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasteridas I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 564)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 TICACTCTCCCTCACTCTCAACACTACACACCCTTAGCTGGCAACATTGCTTGTCCACT 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGTTCTTGAGAAATGCCGTGJJTGCGCCACCACGGACGCCGTCG---CCGAGTTTACAGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 TAAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475 ATTACCACTTTTTGCTTTACAGGTGACGGTGTTCTCCAACACGGTATATGCATTGGACG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 CAATCTTCATCAAGTTCTTGGIGATGCCAGTTCTTTTCTGCATTTTAATAAATTATGGGT 594
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                                                                                                                                                                                                                                                                                                    Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com.
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Pred. No. 3.1e-18;
0; Mismatches 234; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="cSTB13B18"
/clone_lib="potato leaves and petiole
/tissue_type="leaflets and petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="8 weeks old plants'
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism≔"Solanum tuberosum"
/cultivar≔"Kennebec"
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterida I; Solanales: Solanaceae: Solanum.

E 1 (bases 1 to 659)

E 2 van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

L Unpublished (2000)

Contact: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1800-711-6195, email cdna@fresgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xhol; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were trozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                              BG598154 659 bp mRNA EST 12-APR-2001
EST496832 cSTS Solanum tuberosum cDNA clone cSTS20M23 5' sequence,
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGTTCTTGAGAAATGCCGTGTTGCGCCACCGGACGCCGTCG---CCGAGTTTACAGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 CCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 CCCTCTAACTTATTTTGATCTATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 CTACAGATTCCGCCATCCTTGTCCCAACTC - TAAATTTATCATTCATCCATTAAATCG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 TACAAGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTCTTAAAACAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 TCCCTTTCCCTTGTTCTCAAACACTTTCCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 TCACTCTCCCTCACTCTCAAACACTACACCCTTAGCTGGCAACATTGCTTGTCCACTA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 GATTCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 AAT---TCGAGTGGTTATCCTGAGTTGCGTTATGTGACTGGAGATTCTATATCTGTTACT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 ATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGGGGATTCTTAT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 114.6; DB 155; Length 659;
55.0%; Pred. No. 3.2e-18;
tive 0; Mismatches 244; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="grouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4113"
/clone="cSTS20M23"
/clone_lib="cSTS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13F-R
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595 TTTGGTTGACAAA 607
                       ||| | ||||||
552 TTTACTCAACAAA 564
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: ANOi; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and greenhouse grown plants. The tissue was immediately frozen in limid attrocen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B. Generation of ESTS from potato leaves and petioles (unpublished (2000))
Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG097054 508 bp mRNA EST 29-JAN-2001
EST461573 potato leaves and petioles Solanum tuberosum cDNA clone
CSTE45P9 5' sequence, mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                       475
                                                                                                                                                                                                                                          535
382 TTTATTGAGACTGATATGAATTTCAATCGTTGGTAACCATCCTCGAAATGCTAAG 441
                                                                                                                                                                          501
                                                                                                                                                                                                                                                                                                              561
                                                                                                                                                                                                                                                                                                                                                                                                                     125 TCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 GAGAAATGCCGTGTTGCGCCACCGGACGCCGTCG---CCGAGTTTACAGTCCCACTG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
                                                                                                                                                                       442 GATTTTTATCCCTTCATTGCTCAATTGGCACAAGCTAAGGATGCACCGGGGGTCAAACTA
                                                                                                   416 AAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTA
                                                                                                                                                                                                                                       476 TTACCACTTTTGCTTTACAGGTGACGGTGTTCTCCCAACACCGGTATATGCATTGGACGC
                                                                                                                                                                                                                                                                                                           502 GTCCCGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGCATATCCCGTTGGTGT
                                                                                                                                                                                                                                                                                                                                                                              536 AATCT---TCATCAAGTTCTTGGTGATGCCAGTTCTTTTTCTGCATTTTAATAAATTATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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1 (bases 1 to 508)
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/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host-"SOLR"
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0; Mismatches 216
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/organism="Solanum tuberosum"
/cultivar="Kennebec"
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/clone="cSTB45P9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 GTTTTGGTTGACAAATCCAATGGAGAT 619
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Spermatophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Atteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 46.3)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
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                                                                                                                                                                                                                                                                                                                                                                                                240 CATTGGTAACCATCCTCGAAA&GCTAAGGATTT---TTATCCCATTCCTCAATTGGCACA 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTCCTTCCACTTTCTTCTCT.ACCTATGTACGACAGATCTGTGGTGCAAGATCCATTTCA 687
                                                                                                         208 TAAATTTATCATTCATCCATBAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCC 267
                                                                                                                                                268 GTTAGCCGGGAATTTGATTTGCCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTA 327
                                                                                                                                                                                                                                                                       328 CAAGAAAGGGGACTCCGTTTC?TTAACAATTGCAGAATCGAGCATGGATTTTGATTATCT 387
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                     Length 574;
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Division tel 1-800-711-6195, email cdna@resgen.com.
                                                              0; Mismatches 222; Indels
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/db_xref="taxon:4113"
/colone="cSTB34B1"
/clone=lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
                       DB 142;
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                                             Pred. No. 9e-17
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                       Score 108.8;
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The Institute for Genomic Research
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                     6.78;
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                                                              Matches 281; Conservative
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(bases 1 to 574)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Llang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
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The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                419 GTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGCATATCCGTTGGTTTTAGTAAC 478
ACTTATTTTGATCATATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAG 121
                                                                                                                           TCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGATTCC 301
                                                                                                                                                TCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATTGCA
                                                                                                                                                                                                                                               239 TCGAGTGGTTATCCTGAGTTGCGTTATGTGACTGGAGATTCTATATCTGTTACTTTTATT
                                           TTCCGCCATCCTTGTCCCAA----CTCTAAATTTATCATTTCATCCATTAAATCGTCCCTT
                                                                     122 CTACCAATTTCCAAACTCGATTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTC
                                                                                                                                                                                                                                                                                        362 GAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAATTC
                                                                                                                                                                                                                                                                                                                                                                          422 AACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 CTTTTTGCTTTACAGGTGACGGTGTTCTCCAACACCGGTATATGCATTGGACGCAATCTT
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/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dew_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .574
/organism="Solanum tuberosum"
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JOURNAL
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KEYWORDS
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen.
                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                              209 AAATTTATCATTCATCCATTAAATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ATAGGAGACCATCCTAGAAAGGCAAAGGATTTTATCACTTTGTTCCAAAGTTGGCGGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 TTAGCCGGGAATTTGATTTGGCCGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 AAGAAAGGGGACTCCGTTTCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCTC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 GTAACAGGGGATTCTGTGTCAGTTACTTTTTTTTGTGAAAGTGATATGGATTTTCTC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 CC-----GATTGTAACCTCCGGCGACGAAGTATTACCACTTTTGCTTTACAGGTGACG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 GIGTTCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGATGCC 562
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                                                                                                                                                                                                                                                                                                                    9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     11 AAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCGCTCTCCAACCATATAGATT 70
                                                                                                                                                                                                                                                                      Query Match
6.4%; Score 103.6; DB 143; Length 403;
Best Local Similarity 57.6%; Pred. No. 1.7e-15;
Matches 228; Conservative 0; Mismatches 159; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 AGTTCTTTTTGCATTTTAATAAATTATGGGTTTTG 598
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Search completed: November 5, 2001, 18:00:43 Job time: 14883 sec

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TELEPHONE: (703)836-9300
TELEFAX: (703)883-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-463-14
(without alignments)
1819.738 Million cell updates/sec
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Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appl
Sequence 137, Appl
Sequence 1137, Appl
Sequence 186, Appl
Sequence 2, Appli
Sequence 5, Appli
Sequence 90, Appl
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                          November 5, 2001, 18:03:41; Search time 168.74 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuS_COMB.seq:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-783-266-1

US-09-023-327-1

US-08-998-416-1137

US-08-998-416-288

US-08-998-416-186

US-08-998-416-186

US-08-954-659-11

US-09-103-429A-2

US-09-103-429A-2

US-09-103-429-90

US-08-906-616-90

US-08-906-616-90

US-08-906-616-90

US-08-906-616-90

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US-08-613-90

US-08-613-90

US-08-613-90

US-08-06-613-90

US-08-06-613-90

US-08-06-613-90

US-08-06-613-90

US-08-96-613-90

US-08-96-613-90
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US-08-764-100-9
US-08-764-100-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM nucleic · nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                              US-08-894-356C-2
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Query
Match Length DB
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39.6
38
38
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    CONTRACTOR
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                                                                                                                                                                                                                                                                                                                                              65 CTTGAGAAATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTG 124
                                          Gaps
                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Williamson, Valerie M.
APPLICANT: Williamson, Isgouhi
APPLICANT: Williamson, Isgouhi
APPLICANT: Waloshian, Isgouhi
APPLICANT: Waloshou, John
APPLICANT: Milliam Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
NUMBER OF SEQUENCES: 5
CORRESPONDEMECE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
DB 1; Length 7218;
                                        88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTERION NUMBER: US/08/947,823
FILING DATE: 09-0CT-1997
Query Match 2.5%; Score 40.8; DB Best Local Similarity 2.5%; Pred. No. 0.091; Matches 6; Conservative 146; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  023070-070210US
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APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: DNA (genomic) US-08-947-823-1
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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US-08-947-823-1/C
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STATE:
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                                                                                               1513 TTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCAT 1572
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                                                                                                                                                   1472 TAAGAAAAAAGTGGTATCAATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTT 1531
                                          Gaps
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Score 39.6; DB 3; Length 51952;
Pred. No. 0.57;
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                                        Indels
                                        :69
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                                        0; Mismatches
                                                                                                                                                                                                                                          32534 ATATTCCTTCAAAACATGTCAAAACAAA 32505
                                                                                                                                                                                                                          1592 CAATTGTTTTAAAAAAAAAAAAAAAAAAAA 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/463,975
FILING DATE: JUNE 5, 1995
CLASSIFICATION ATA:
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 21 OCT 1994
ATTORNEY, AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 35.134
REFERENCE/DOCKET NUMBER: 325800-331
TELECHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GII
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08463975; Patent No. 5618717; GENERAL INFORMATION:
APPLICANT: WEI, ET AL.
TITLE OF INVENTION: hABH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
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59.1%;
       2.4%;
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       Query Match 2.4%
Best Local Similarity 54.0%
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201-994-1744
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LI
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07068
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                                                                                                                                                                                                                                                                                                                                      US-08-463-975-1
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Weller S. Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND FLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1513 TTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCAT 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3%; Score 38; DB 2; Length 1953; 59.1%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Knobbe Marténs Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,975
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 21 OCT 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARG, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DGS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1953 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 59.1
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 201->2.
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 620 Newport
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                       NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINEAR
                       ROSELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: LII; MOLECULE TYPE:
US-09-023-327-1
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                     ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92660
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                                                                COUNTRY:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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59.1%; Pred. No. 0.29;
tive 0; Mismatches 45; Indels
                                                                                                                          GENERAL INFORMATION:
APPLICANT: WEI ET AL.
TITLE OF INVENTION: DABH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CERELA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GREEN AND THE TALL APPLICANT: WEI, ET AL.
TITLE OF INVENTION: habh
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,266
FILING DATE: 15.4AM.1997
CLASSIFTCATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: JUNE 5, 1995
APPLICATION NUMBER: PCT/US94/12058
FILING DATE: 10CT 1994
ATTONNEY,AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: 35,334
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-023-327-1
; Sequence 1, Application US/09023327
; Patent No. 5929225
                                                                                     Sequence 1, Application US/08783266
Patent No. 5747312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1700
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1953 BASE PATRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.3 Best Local Similarity 59.1 Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-08-783-266-1
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APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
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Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1692RP
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 LENGTH: 636 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                              SEQUENCE CHARACTÈRISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.3
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 ATTAATAAATAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-998-416-288/C
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
UNUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREFT: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%; Score 38; DB 2; Length 191
Best Local Similarity 53.3%; Pred. No. 0.97;
Matches 80; Conservative 0; Mismatches 70; Indels
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 105/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERBUCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-8550
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 15806 AAATTTATATTTAAATAAAAAAAAAATAAA 15835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1593 AATTGTTTTAAAAAAAAAAAAAAAAAAA 1622
                             CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1137, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-998-416-1137/C
                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
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US-08-487-826B-13
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1550 ATGGGAAGATGTATCAAACTCATCTCTATATATATATATTCAATTGTTTTAAAAAAA 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score 37.6; DB 4;
55.3%; Pred. No. 0.21;
tive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Pohlmann, Rainer
APPLICANT: Pohlmann, Rainer
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corline
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carollna
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.3%; Score 37.6; DB 4; Length 837; Best Local Similarity 55.3%; Pred. No. 0.24; Matches 73; Conservative 0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFICATION: 435
                                                     PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: No. 6239264artis Corporation STREET: 3054 Cornwalls Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-998-416-186/c
; Sequence 186, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
            NAME: Me199, J. TIMOCHY
REGISTRATION UNUBER: 38.241
REFERENCE/DOCKET NUBBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
21P: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                       ; ORGANISM: PAG1241RP
US-08-998-416-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1610 AAAAAAAAAA 1621
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1495 ATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGGG 1554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPUTER: DATE: PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.4; DB 4;
Pred. No. 0.23;
0; Mismatches 56;
PF/5-30306/A/CGC1976
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                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-869
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTER.STICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 436
ATTORNEY/ACENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genemic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%;
Best Local Similarity 55.5%;
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 575 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: PAG1074RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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ZIP: 11530-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1615 AAAAAAA 1621
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FEATURE:
NAME/KEY:
LOCATION: 1444..1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 4160
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                                                                                                                                                                                                                                                                                   US-09-341-678-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                          1434 CGAATTTCATCAATAGTCTCCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATG 1493
                                                                                                                                                                                                                                                                                   1494 TATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCCATGG 1553
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Granados, Robert R
APPLICANT: Granados, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: cDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                         ;
0
                                                                    Score 37; DB 1; Length 575;
Pred. No. 0.29;
0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOURT: IN TOPY COMPATIBLE
COMPOURTS: IN PC COMPATIBLE
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
CITY: Ithaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MICHAELS, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTT-39
TELECOMUNICATION INFORMATION:
TELEPHONE: (607) 256-200
TELEFAX: (607) 256-368
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2821 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Trichoplusia ni

DEVELOPMENTAL STAGE: larva

11SSUE TYPE: peritrophic membrane

US-09-103-429A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09103429A; Patent No. 6187558; GENERAL INFORMATION:
DNA (genomic)
                                                                    Query Match 2.3%;
Best Local Similarity 49.7%;
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGI.
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                          1614 AAAAAAAA 1622
                                                                                                                                                                                                                                                                                                                                                                                           561 AAAAAAAA 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
; MOLECULE TYPE:
US-08-554-659-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-09-103-429A-2
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                                                                                                1521 CAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCATCTCTCTAT 1580
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                                                                                                                                            2721 CAACAAATGGTTAAGAAAAAAAAGGATTTCTTAAAAATGTATTATTATAAAATGTGTAA 2780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MAKAR17
LOCATION: 945..968
OTHER INFORMATION: region corresponding to oligonucleotide MAKAR17
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Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                  40; Indels
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: RARMI, MANSOUR
APPLICANT: BARTHELS, Nathalie
APPLICANT: GHEYSEN, Godelieve
TITLE OF INVENTION: PATHOGEN-INDUCED PLANT PROMOTERS
FILE REFERENCE: 621-0014
CURRENT APPLICATION NUMBER: US/09/341,678
CURRENT FILIGATION NUMBER: PCT/EP98/00388
EARLIER APPLICATION NUMBER: PCT/EP98/00388
EARLIER PILIG DATE: 1998-01-19
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 2.2%; Score 36.4; DB 4;
Best Local Similarity 58.2%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION: 1418..1570
OTHER INFORMATION: putative open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: insertion point of T-DNA OTHER INFORMATION: insertion in the line ARM1
                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 90, Application US/08906769 Patent No. 6077687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09341678 Patent No. 6252138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Ru Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
    Query Match 2.3%;
Best Local Similarity 60.4%;
Matches 61; Conservative
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1439 TTCATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATGTATAA 1498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 TTTACCAATGTTGCTCATTTRGTGGATTGGATTCAAGAACATACTGGATTGGAATTGTAA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                769 AAATAAAACTCAAACTAAAAAAAAAATAATTTAATTGCACTGAAAAATTTTTCAAGAAAA 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "At pos. bp 560, change G to
N. At pos. aa 187, substitute Xaa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 2.2%; Score 35.8; DB 3; Best Local Similarity 49.7%; Pred. No. 0.81; Matches 91; Conservative 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUTURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORREY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 25.020
REGISTRATION NUMBER: 25.020
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-02.3
INFORMATION FOR SEQ ID NO: 90: SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
                                                                                                                                                                                                                     1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-817-795-90
; Sequence 90, Application US/03817795
; Patent No. 6139840
; GENERAL INFORMATION:
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Gaines, Patrick J.
TILLE OF INVENTION: FLEA AMINOP
NUMBER OF SEQUENCES: 190
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                         Sheridan Ross P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Grieve, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: ; OTHER INFORMATION: ; ; OTHER INFORMATION: h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                        Colorado
: USA
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                                                                                                                                                                                                                                                     Denver
                                                                                                                                                                                                                                                                                          COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              769 AAATAAAACTCAAACTAAAAAAAAAATAATTTAATTGCACTGAAAAATTTTCAAGAAAA 828
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49.7%; Pred. No. 0.81;
Live 0; Mismatches 92; Indels
                                            FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "At pos. bp 560, change G to N. At pos. aa 187, substitute Xaa."
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                     NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-906-616-90
; Sequence 90, Application US/08906616
; Patent No. 6121035
; GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
    Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 49.7
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATION: 1.,766
CTHER INFORMATION:
CTHER INFORMATION:
US-08-906-769-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                    APPLICANT: Silver,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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: USA
                                                                                                                                                                                Denver
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1619 AAA 1621
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                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                             CITY: 1
STATE:
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APPLICANT: Arisen, Ann.
APPLICANT: Dale, Beverly
APPLICANT: Dale, Beverly
APPLICANT: Dale, Beverly
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
CORRESPONDENCES: 119
CORRESPONDENCE ADDRESS:
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Pred. No. 0.81;
0; Mismatches 92; Indels
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CITY: Denver
STATE: COlorad
COUNTRY: USA
2 IP: 80203
COMPUTER: USA
2 IP: 80203
COMPUTER: ENADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GARY J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELEPHONE: (303) 863-9700
TELEPAX: (304) 863-9700
TELEPAX: (304) 863-9700
TELEPAX: (305) 863-9700
TELEPAX: (306) 863-9700
TELEPAX: (307) 864-9700
TELEPAX: (308) 863-023
INFORMATION FOR SED ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
                   Hunter, Shirley Wu
Frank, Glenn R.
Heath, Andrew W.
Yamaka, Miles Yamanaka
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Rushlow, Keith E.
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Best Local Similarity 49.79
Matches 91; Conservative
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LOCATION: 1..766
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STREET: 17
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Db 889 AAA 891
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Search completed: November 5, 2001, 18:04:15 Job time: 15055 sec

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Malaria-specific g SERP gene. Plasmo Sequence encoding CDNA encoding Plas Full length human

BAC containing rep Human lung tumour

Human cancer assoc Nucleotide sequenc Nucleotide sequenc Human TGF-beta rec Nucleotide sequenc Nucleotide sequenc

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Sequence:

Title:

Searched:

Database

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Result Ş

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Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
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//product= Aromatic acyl transferase.
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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tone,
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       CTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGGTAGAT
                                         183 ctctctaaaactctcatacacttcttccctctctcatgcaatttaatctacccttca---
                                                                                                                                                                       360 ctctacaactttgtccctaaattgccgcccattgtcgaagaatccgatagaaaactcttc
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                                                                                                                  GCAGAATCGAGCATGGATTTGATTATCTCGCCGGAGATCATCAGAGGGATTCTTATAAA
                                                                                                                                                                                                                            TTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTA
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                                                                              299 TCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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/*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                                  Aromatic acyl transferase coding sequence.
                                           ВР
                                         standard; cDNA to mRNA; 1479
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                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                Perilla ocimoides (Clone pSAT208)
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Nakao M, Tanaka Y, Yonekura K;
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P-PSDB; AAW04725.
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TCAAAGTTCTTGAGAAATGCCGTGTTGCGCCACCACCGGAC---GCCGTCGCCGAGTTTA 113

Score 190.8; DB 17; Length 1703; Pred. No. 3e-39;); Mismatches 617; Indels 48;

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AATCGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGC 290

CGGTAGATTCCTCCGATAGAATGCCGGAGTTGCGTTAC-----AAGAAAGGGGACTCCG 344

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TITCTTTAACAATTGCAGAATCGAGCATGGATTTTGATTATCTCGCCGGAGATCATCAGA 404 taactitgatcgttgcggagtctgaccaggattitgactaccitaaaggicatcaactgg 381 GGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACC---T 461 tagattccaatgatttgcatggccttttttatgttatgccacgggttataaggaccatgc 441 462 CCGGCGACGAAGTATTACCACTTTTTGCTTTACAGGTGACGGTGTTCTCCAACACCGGTA 521

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1439 TICATCAATAGICTCCCATGIGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATGTATAA 1498
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                                                                                      GAGCTTGGCATTTCTTTGCCTAAGAATAGGATGGACGCATTTTGCCACCATTTTTACGAAT
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ura K;
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Nakao M, Tanaka Y, Yonekura
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                                                           atcttcttccatctttcgatagatcgataatcaaagatctgtatggcctagaggaaacat 678
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                                tagccgtggctctgacggcacatcattcaattgcagatgctaaaagttttgtaatgttca
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                                                                                                                                                                                  1299 AAAAGCAIGAAICIGITICAACIAAICCITCGGCAACACIAAITITGAICICICGGICCA
                                                                                                            1239 TTGGATCCGCACAACGCAATGTGCATGATTTTGATGCAGATTTTGGGTTGGGGAAAGCTTG
                                                                                                                                                 CCGCCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAG
                                             cagctattggagaagccattgaaaagaggttgcacaacgaaaaggcgttcttgcagatg
                                                             1179 ATTGGATATCGCCGCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCG
                                                                                caaaaaacttggttatcggaatctaat-----ggaatcccttcaaaaagatttctcg
                                                                                                                                                                                                                                                                                                                                                  Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding for aromatic acyl transferase – for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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/product= Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fukui Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAM37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727. however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAM04727 that the indexer decided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGCCGTGTTGCGCCACCACCGGACGCCGTCGCCGAGTTTACAGTCCCACTGTCGTTTT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17; Length 1518;
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Pred. No. 8.4e-30;
0; Mismatches 642;
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826 tctggaccggcatcgccaaat-----cggtcggagattacaaagacgtggatgacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 tatctcttactttcttcgacattacttggctactcttccctccggtccaccatcttttct 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                              plants
tone,
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                                                                                                                                                                                                                                                                                                                                                                       DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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                                                                                                                                                                           Kusumi T,
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                                                                                                                                                                           Fukui Y,
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95JP-0067159.
95JP-0196915.
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                                                                                                        (SUNR ) SUNTORY LTD
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                                                                                                                                                                  TAAGAGAAGATGGAAGAGGATAAACATGCAGCAAACTTATGTGCTTTCATCAACTGCC 1001
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                                                                             gtcccactgataaagttcggtcaacgtttgtgtttgacccgaactaatatcaatctactaa
                                                                                              AGAAATTCATTTCGTCAAAAATCGCAACTTAACCGGTAGTAGTAATTATAATCTGTCAA
                                                                                                        gatetegtettgatecaecaatteecaeageetaetttggtaaetgtggtgeaecatgtg
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       TCTACAATGAAAGAAAACTGCTCAAATCTCAGGGCACACCTACTGTTCTAAATCCAGCAA
                                         643 atgaaaataagttgagacatacaaggctcgaaagtttttataaaccttcgagccttgttg
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                                                           TTTCTAAAGATGAAGTTCGAGCCACCTTCATCCTACACCCTATTGATATCATGAAGCTCA
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                   26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                         26-JUL-2000; 2000WO-US20476
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1517 GATGCAACAAATGTTTTAGGAGATTACAAATCCATGGGAAGATGTATCAAACTCATCTCT 1576
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                857 GGTAGTAGTAATTATAATCTGTCAACTTTCACGGTGACATCTGCACTGATCTGGACATGC 916
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                                                                     Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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2000US-0190259.
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1037 ITTGGAAATTGCATAGTGCCTTGTATGGTGGGATCGACTCATGAGCAACTTGTAGGAAAT 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGTGCATGATTTTGATGCA 1276
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                          The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                            GGTAGTAGTAATTATAATCTGTCAACTTTCACGGTGACATCTGCACTGATCTGGACATGC 916
                                                                                                                                                                                                                                                                                                                                                                                                                                        431
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.0%; Pred. No. 2.8e-15;
.ve 453; Mismatches 305;
                                                                                                                                  Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                         Example 6; Page 127; 159pp; English.
                                                                                                                                                                                      Conservative 453;
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Best Local Similarity 1.0%;
Matches 8; Conservative 4
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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L.0%; Pred. No. 2.8e-15;
Lve 453; Mismatches 305;
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17-MAR-2000; 2000US-0190259
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Best Local Similarity 1.0%;
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AAF58259/
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Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

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1217 AGGTCGACGCTCATTTATGTCGTTGGATCCGCACAACGCAATGTGCATTTTGATGCA 1276
                                            1277 GATTTTGGTTGGGGAAAGCTTGAAAAGCATGAATCTGTTTCAACTAATCCTTCGGCAACA 1336
                                                                                       1337 CTAATTTTGATCTCTCGGTCCAGAAGATTTAAAGGAGCACTTGAGCTTGGCATTTCTTTG 1396
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                                                                                                                                               The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) monitoring gene expression.
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                 1397 CCTAAGAATAGGATGGACGCATTTGCCACCATTTTTACGAATTTCATCAATAGTCTCCAT
                                                                                                                                                                                                                                              Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259
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            936;
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           22;
 Score 96.8; DB 2
                     llarity 1.0%; Pred No. 2.8e-
Conservative 453; Mismatches
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Query Match
Best Local Similarity
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
1397 CCTAAGAATAGGATGGACGCATTTTGCCACCATTTTTACGAATTTCATCAATAGTCTCCAT 1456
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                                                                               128 TTTTCGACATGCGATGCTTGATCTCTGATGCAGAACACCATCTGCATTTCTACAGATTC 187
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Matches 12; Conservative 451;
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17-MAR-2000;
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17-MAR-2000; 2000US-0190259.
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gene expression; ss.
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Pred. No. 6.3e-15;
11; Mismatches 312;
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                                                                                                                                                        Example 6; Page 127; 159pp; English
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WPI; 2001-159728/16
                                                                                                          single surface
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                428 TTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGACGAAGTATTACCACTTTTT 487
                                   488 GCTTTACAGGTGACGGTGITCTCCAACACCGGTATATGCATTGGACGCAATCTTCATCAA
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Matches 12; Conservative 451; Mismatches 312;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                         Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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Search completed: November 5, 2001, 18:11:26 Job time: 15421 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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HLHFYRERHEOPNSKF1SSIKSLSLUKHFLPLAGNLIWPVDSSDRMFELFYKGD
SVSTTIAESSMDFDVLAGDHQSYKFNDLIPOLPREIVTGEDSLPRYKKGD
SVSTTIAESSMDFDVLAGDHQSYKFNDLIPOLPREIVTGEDKLEPLSLEPWDRSVODFFH
TGICIGRNLHQVLAGDASSFLHFNKLWVLVDNSNGSDEKFLPLSSLPRYDRSVODPFH
IRRKIYNERKLLKSOGTPYLNPAISKDEVRAFTILHPIDIMKLKFISSKNRNLTGS
SNYNLSTF"VYSALIWTCLSKSLDTVVREKVEEDKHAANLCAFINCRQRFAPPIPQNY
FGNOIVPCNYOGTHPOLVGRGESLSVAATAIGDAIHKRLHDYEGILRGDWISPPRSTSA
APRSTLITVVGSAQRNVHDFDADFGGGKLEKHESVSTNPSATLILISRSRRFKGALEL
GISLDRNRNDAFATIFFHRSLHVRSPL"

78 a 345 c 322 g 477 t
                                                                                         Unpublished (1999)
2 (bases 1 to 1622)
3 (bases 2 to 1622)
4 (bases 3 to 1622)
5 (bases 3 to 1622)
Yonekura-Sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M., Eujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T. Molecular cloning and biochemical characteization of hydroxycinnmamoyl-Coa.anthocyanin
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/db_xref="taxon:55190"
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Gentiana triflora cDNA to mRNA.

Gentiana triflora triflora

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI,
                                                                                                                                                                                                                                                                                                                                         l (bases l'to 1479)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 4 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1479;
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product='acyltransferase'
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/organism="unidentified"
/db_xref="taxon:32644"
a 316 c 331 g 41:
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17-FEB-1995 JP 95P 671
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strandedness: Double;
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JP 1997070290-A/4
18-MAR-1997
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JP 1997070290-A/4.
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Perilla frutescens leaf CDNA to mRNA.
Perilla frutescens
Edwaryota, Virfaliplantaes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts;
Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko
Sakakibara, Suntory Research Center, Fundamental Research, Plant
Biotech; Shimamoto-cho, Wakayamadai, 1-1-1, Mishima-gun, Osaka
618-65/03, Japan (E-mail:Reiko_Sakakibara@suntory.co.jp,
Tel:+81-75-962-8807, Fax:+81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA 04-APR-2000 for anthocyanin acyltransferase, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukui, Y.
                                                                                                                                                                                                                                                                               ATTGATGGGGAGAAATATGCAATGACRCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTG 1268
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                                                                     GAGCTTGGCATTTCTTTGCCTAAGAATAGGATGGACGCATTTGCCACCATTTTTACGAAT
                                                                                                      1439 ITCATCAATAGTCTCCATGTGAGGAGCCCTTTGTAAGAAAAAGTGGTATCAATGTATAA
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Sakakibara,K.Y., "anaka,Y., Mizutani,M.F., Fujiwara,H., I
Ashikari,T., Yamaquchi,M. and Kusumi,T.
Molecular and biochemical characterization of a novel
hydroxycinnamoyl_coA: anthocyanin 3-0-glucoside-6
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/protein_id-"BAA93475.1"
/db_xref-"GI:7415646"
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/db_xref="taxon:48386"
/tissue_type="leaf"
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Sakakibara, K.Y. and Tanaka, Y.
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anthocyanin acyltransferase.
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Perilla frutescens mRNA
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TTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCTCCGGCGAAGTATTA 478
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                                          AGATTCCGCCATCCTTGTCCCAAC - - - TCTAAATTTATCATTCATCCATTAAATCGTCC
                                                                                                                            CTCTCTAAAACTCTCATACACTTCTTCCCTCTCATGCAATTTAATCTACCCTTCA---
                                                                                                                                                          TCCTCCGATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACTCCGTTTCTTTAACAATT
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GDSITLIVAESDODFDYLKGHOLVDSNDLHGLFYVMPRVIRTWODYKVIPLVAVQVTV
PPNRGIAVALTAHHSIADAKSFVMFINAMAYINKFGKDADLLSANLLPSFDRSIIKDL
YGLEETFWNEMODYLENFSRFGSKPPRFNKVRATYVLSLAEBIOKLKNVLNLRGSEPT
INTIFTHATOXYWTCWYKSKDDVYSESSNDENELEYFSFTADCRGLLTPPCPPNYF
GNCLASCYAKTHREUGUKGLLLYANAAIGERIEKRHHNEKGYLADAATWLSESNGIP
SKRFLGITGSPKFDSYGVDFGWGKPAKFDITSVDYAELIYVIOSRDFFEKGVEIGVSL
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SLLFYDFPYPFTHFLDTVIPNLKASLSLTLKHYVPLSGNLLMPIKSGEMPKFQYSRDE
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Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fukuchi-Mizutani,M., Nakao,M., Fukui,Y., Yamaguchi,M., Ashikari,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB010708 1679 bp mRNA PLN 20-FEB-1999
Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (22-JAN-1998) to the DDBJ/EMBL/GenBank databases.
Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research;
1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan
(E-mall:Hiroyuki_Fujiwara@suntory.co.jp, Tel:+81-75-962-8807,
  --GTTGCAGAAATCATATTTTCGGTGGCAGGATCGAGCAAG 1148
                                                                                              1149 CTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAGCAAGAATATTGTCG 1208
                                                                                                                                                                                           ATTGATGGGGAGAATATGCAATGACACTTTGTAAAGCCAGGGATTTCGAAGGAGGATTG 1268
                                                                                                                                                                                                                                                                   cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora Plant J. 16 (4), 421-431 (1998) 99097837
                                            GTGCATGATTTTGATGCAGATTTTGGTTGGGGAAAGCTTGAAAAGCATGAATCTGTTTCA
                                                                                                                                              ACTAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCAGAAGATTTAAAGGAGCACTT
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/product="Anthocyanin 5-aromatic acyltransferase"
/protein_id="BAAA74128.1"
/db_xref="GI:4185599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anthocyanin 5-aromatic acyltransferase.
Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
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/db_xref="taxon:55190"
/clone="pGAT4"
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6. .1415
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C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
GIATGGTGGGATCGACTCATGAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAA 1118
                         GCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTG 1086
                                                                 1087 CAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACAACAAAAAGGCGTTCTTGCAGATG 1146
                                                                                                                                                                  TIGGAICCGCACAACGCAA'TGTGCAIGAITITGAIGCAGAITITGGITGGGGAAAGCTIG 1298
                                                                                                                                                                                                                        1299 AAAAGCATGAATCTGTTTCAACTAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCA 1358
                                                                                                                                                                                                                                                                              PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691:
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                      CAAAAACTTGGTTATCGGAATCTAAT-----GGAATCCCTTCAAAAAGATTTCTCG
                                                                                                                                                                                   CCGCCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAG
                                                                                                            1179 ATTGGATATCGCCGCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCG
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/product-'acyltransferase precursor'
9. 1412
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Ashikari,T. Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 1 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     E12753 1703 bp DNA PAT 2
Gentianatriflora mRNA acyltransferase, complete cds.
E12753 1 G1:3251585
JP 1997070290-A/1.
unidentified.
unidentified.
unidentified.

    1703
/organism='Gentianatriflora'
/vartety='japonica'
/tissue_type='petal'
/clone='pGAT4'

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/db_xref='taxon:32644"
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strandedness: Double;
topology: Linear;
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                                       48;
          Length 1679;
                                       Indels
          Score 189.2; DB 12;
Pred. No. 7.8e-37;
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        Ouery Match
Best Local Similarity 52.2%;
Matches 728; Conservative
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                                      Length 1703;
                                     Score 189.2; DB 10; Length
Pred. No. 7.9e-37;
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ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
                                                                 GTATGGTGGGATCGACTCATGAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAA
                                                                                                                                                   1119 CCGCCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAG
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 5 18-MAR-1997;
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/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type='petal'
/clone='pCAT48'
1.1367
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JP 1997070290-A/5
18-MaR-1997
30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 67159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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(C12N9/10,C12R1:19);
strandedness: Double;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E12757 1508 bp
Senecio cruentus mRNA
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JP 1997070290-A/5.
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Hyman R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
Submitted (21-JUL-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, CA
94304, USA
                                                                                                                                  CCATCGGAGATGCTATCCNTAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAGTT 1181
                                                                                                                                                     1102 CGAGATGGCATGAACCTTTPCATGATCCCGG------CTAGGAAGATTGGTGTTGCTG 1152
                                                                                                                                                                                                                                                                                    GATCCGCACAACGCAATG%GCATGATTTTGATGCAGATTTTTGGTTGGGGAAAGCTTGAAA 1301
                                                                                                                                                                                                                                                                                                       1302 AGCATGAATCTGTTTCAACTAATCCTTCGGCAACACTAATTTTGATCTCTCGGTCCAGAA 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 178273: contig of 178273 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 178273)
 GATCTCGTCTTGATCCACACAATTCCCACAGCCTACTTTGGTAACTGTGGTGCACCATGTG
                                                                                             982 TCCCGACCTTAAAAAATG!CGTTTTGACTAGCGAAAATGGGTATGCACTTGGTGCTAAAG
                                                                                                                                                                                                            1182 GGATATCGCCGCCCCGGATCAACATCTGCGGCACCAAGGTCGACGCTCATTATGTCGTTG
                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGGATCGACTCATGAGCAACTTGTAGGAAATGAAGGGTTGTCGGTAGCTGCAACCG
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On Aug 12, 2000 this sequence version replaced gi:8810450.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromoscme="12"
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HTG; HTGS_PHASE2.
malaria parasite P. falciparum.
Plasmodium falciparum
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/clone="3D7"
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TITLE
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                                                                                                                                                                                                                             TCCCACTGTCGTTTTTCGACATGCGATGGTTGATCTCTGATGCAGAACACCATCTGCATT 176
                                                                                                                                                                                                                                                                                                    TCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAAC 180
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                                                                                                                                                                                                                                                   CGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTTGATTTGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 AGAGGGATTCTTATAAATTCAACGATTTGATTCCGCAGCTGCCAGAACCGATTGTAACCT
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                                                                                                                72;
                                                                           Length 1508;
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                                                                           DB 10;
                                                                                                              0; Mismatches 642;
                                                                         Score 139.8; DB 1 Pred. No. 1.9e-24;
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                                                                                             Similarity
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 4 unordered places.
                                                                                                                                                                       76638 AATAAATAAAATAAAATAAAATATATTGTTAAAAAAAGAATTCCGAATTTTTAAATGC 76579
                                                                                                                                                                                                                                      76578 TITAAAAAATGTCAAAAATATTATATTTATGAATATTTTACAAAAATTTGGGAAAAAAT 76519
                                                                                                                                   1490 AATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAGGAGATTACAAATCC 1549
                                                                                                                                                                                                               1550 AIGGGAAGAIGTAICAAACTCAICTCTCTAIATAIATAITAIATTGIITTAAAAAAA 1609
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC005506.8 GI:9797717
HTG: HTGS_PHASE1.
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (Dases I to 205429)
1 (Dases I to 205429)
Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [ Fases 1 to 205429)
Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
                                                      Length 178273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; Score 50.2; DB 60; Length 205429; 58.3%; Pred. No. 0.11; Live 0; Mismatches 63; Indels 0;
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                                        Score 50.4; DB bu; Pred. No. 0.095; Indels
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132469: gap of unknown length
19227: contig of 59758 bp in length
192427: gap of unknown length
203864: contig of 11437 bp in length
204064: gap of unknown length
205429: contig of 1365 bp in length.
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                                                                                              0; Mismatches
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                                                        3.1%;
                                                Ouery Match
Best Local Similarity 61.47
Matches 81; Conservative
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Best Local Similarity 58.3
Matches 88; Conservative
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AUTHORS
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Submitted (16-MAY-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 2304, US.

On Aug 12, 2000 this sequence version replaced gi:8810452.

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                          Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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                                                                  1476 AAAAAAGTGGTATCAATGTATAAAAAAGACAGACAAGTTATGATGCAACAAATGTTTTAG 1535
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Plasmodium falciparum.

Plasmodium falciparum.

Plasmodium falciparum.

I (bases 1 to 169794)

Hyman, R.W. Fung-P.E.., Qin, F., Rowley, D., Mao, J., Tamaki, T., Ruzdi, O.B., Conway, A.B. and Davis, R.W.

Plasmodium falciparum 3D7 chromosome 12
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Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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830 44029: gap of unknown length
030 87202: contig of 43173 bp in length
403 87402: gap of unknown length
825 95024: contig of 7422 bp in length
025 169794: contig of 74770 bp in length
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/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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Pred. No. 0.12;
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atb6 gene; atb9 gene; Arpase Subunit 6; Arpase subunit 9; cob gene; cox1 gene; cox2 gene; cox3 gene; cytochrome b; cytochrome oxidase subunit 1; cytochrome oxidase subunit 1; cytochrome oxidase subunit 2; cytochrome oxidase subunit 3; nad1 gene; nad2 gene; nad3 gene; nad4 gene; nad5 gene; nad6 gene; nad6 gene; nad6 gene; nad6 gene; nad6 gene; nad6 gene; nad8 ge
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlorococales; Scenedesmaceae; Scenedesmus.

I (bases 1 to 42781)
Kuck, U., Godehardt, I. and Schmidt, U.
A self-splicting group II introm in the mitochondrial large subunit
FRNA (LSURRNA) gene of the eukaryotic alga Scenedesmus obliquus
Nucleic Acids Res. 18 (9), 2691-2697 (1990)
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KNLYYNLLFKKCKDYSKDSFFCIFYNIKKSLL"
                              16S ribosomal RNA; 16S rRNA gene; 23S ribosomal RNA; 23S rRNA gene;
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Whither,W. and Kuck,U.
The group IIB intron from the green alga Scenedesmus obliquus mitochondrion: molecular characterization of the in vitro splicing
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Kuck, U., Jekosch, K. and Holzamer, P.

DNA sequence analysis of the complete mitochondrial genome of the green alga scenedesmus obliquus: evidence for UAG being a leucine and UCA being a non-sense codon

Gene 253 (1), 13-18 (2000)
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Submitted (05-MAY-2000) Jekosch K., Ruhr-Universitaet Bochum, I luer Allgemeine und Molekulare Botanik, Universitaetsstr. 150, D-44780 Bochum, GERMANY
On May 23, 2000 this sequence version replaced gi:7573226 gi:7160201 gi:7619793 gi:7573572 gi:13633.

Location/Qualifiers
1. 42781
/organigm-"Scenedesmus obliquus"
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Botanik, Ruhr-Universitaet Bochum, Postfach 10 21 48,
Universitaetsstr:150, D-44780 Bochum
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/db_xref*"GI:7711034"
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/gene="crf76"
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/transl_table=22
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/gene="tENA-Ile"
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5 (bases 1 to 42781)
Jekosch, K.
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Submitted (21-MAY-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Apr 2, 1999 this sequence version replaced gi:433713.

* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
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malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida: Plasmodium.
1 (bases 1 to 196149)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B.
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Scenedesmus obliquus complete mitochondrial genome.
X17375 AJ271733 AJ272528 AJ277429 AJ400708
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47632 47831: gap of unknown length
47832 179129: contig of 131298 bp in length
179130 179329: gap of unknown length
179330 196149: contig of 16820 bp in length.
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/db_xref="taxon:5833"
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                                                             1596 TGTTTTAAAAAAAAAAAAAAAAAA 1621
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                                                                                                                                                                                                                                                                                                                             , 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                              AC004709.3 GI:4558585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 196149)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                            AC004709
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ACCESSION
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AC004709/c
                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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ORIGIN

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Scenedesmus obliquus strain UTEX 78 mitochondrion, complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1476 AAAAAAGTGGTATCAATGTATAAAAAAGACAGACAAGTTATGATGATGCAACAAATGTTTTAG 1535
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1596 TGTTTTAAAAAAAAAAAAAAAAA 1620
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Best Local Similarity
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AF204057
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WVGAVTSLMRRTMGLVQNDVKRVIAYSTCSQLGYMVVALSLSHYGLAMYHLMTHACFK
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join/forc
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YREGLITNHLTSVGLSYWVRDDGSLQKNNEIILRTMGFTQKENIQIVEELNRFFKLNS
                                                                                                                                      1 (bases 1 to 42919)
Nedelcu,A.M., Lee,R.W., Lemieux,C., Gray,M.W. and Burger,G.
The complete mitochondrial DNA sequence of scenedesmus obliquus
reflects an intermediate stage in the evolution of the green algal
                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (11-NOV-1999) Departement de Biochimie, Universite de
Montreal, 2900 Boulevard Edouard-Montpetit, Montreal, Quebec H3T
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/gene="rnl_d"
/note="Group IIB; not present in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note-"Group IA1; not present in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="rnl_a"
/note="simllar to Escherichia coli sequence"
/product="large subunit ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Escherichia coli sequence"
                                                                           Mitochondrion Scenedesmus obliquus
Bukarryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlorococcales; Scenedesmaceae; Scenedesmus.
( bases 1 to 42919)
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/gene="trnA(ugc)"
join(859. .1871,2480. .2528,3802. .4158)
/gene="rnl_d"
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/organism="Scenedesmus obliquus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organelle="mitochondrion"
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1. .716
                                                                                                                                                                                                                mitochondrial genome
Genome Res. 10 (6), 819-831 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="trnA(ugc)"
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/gene="orf215"
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/gene="orf215"
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786. .858
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859. .1871
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                  AF204057.1 GI:8099190
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                                                           obliquus
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                                      KEYWORDS
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ALO35475. G GI:6562702
HTG; DNA polymerase alpha; DnaJ; flap exonuclease; protein phosphatase; replication A protein; ribosomal processing protein; ribosomal protein; rifin; transcription factor; var. malaria parasite P. falciparum.
[SM Plasmodium falciparum.
[SM Plasmodium falciparum.
[SM Plasmodium falciparum.
[SM Plasmodium falciparum.
[SM Plasmodium, plasmodium.
[SM Devlin, K., Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.

Direct Submission

NL Submitted (24-FEB-1999) P. falciparum Genome Sequencing Consortium, plasmodium, plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I HEDI NQNGNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSKPDDNKSNSVFVINGTRTNRITYNY ENTIRQKKHPENYKYVT I TY SAK YDDNIK EIKRK YE ENYTHFRASYLCHDDLLNITKOT I MFYKKHRELAY RYNYLELGEHKNKDNI I FIREINGLRSTILSEDKTNMEIKRDDFYKYTI I GYTHQCFKDKENYNPVDIMNIHKDIY NDNATNINKEDDDNNYLDMBIKDDESYKII I QYTHQCFKDKENYNPVDIMNIHKDIY NDNATNINKEDDDNNYLDMBIKDDESYKII I GYTHQCFKDKENYNPVDIMNIHKDIY NDNATNINKEDDDNNYLDMBIKDDESHKII
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SGDINICLGNNVKGEDHTFVNMPYDKKKWNEIRKSTNNNYNNINRDKRNTHRSLKNVR
IINIKHKNISYVICKNYLKKGKNYYERRMLKNMNLKYNILKINKYILSCNNIYKYAKM
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NKEKPNDDINIVKMKKRRTYIFINKTYKLFIHNYKNISFKFENLMRKHFVAKYDYIF
KKLSYYITLKKEIDLCKLYMYDMNALEILDKNLDIHIKENKLIQNLHCTINLREIENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDQHKNILEICGKNDISKEETKEHANVLLGCAKTEKEEKNLVDD
KIYNEKSNLINIINNKNDIMKTTDVKNDKTLKDDTIERINOKVVKTKKNHLINEEEKN
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KKNITNEKMELEKEIKNFSNEKITIEKEKONISNDKITLEKEIONIRNEKMTLEKEIO
NISNDKITIEKEIKNFRNDKITLEKEIKNFRNDKMTLEKEIKNFSNDKITLEKEIONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Dec 12, 1999 this sequence version replaced gi:5731898.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is not the entire insert of clone MAL4P2. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRQLFHLEYSKIHSRLFKSLHEWETNKYIFLNQKKKENTQNDHISRLEVLINQSIKIE
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> 1130 aa, contains NKSKPDD repeat sequence"
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)-tract upstream of MAL4P2.01"
Plasmodium falciparum MAL4P2, complete sequence
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/db_xref="taxon:5833"
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5644. .6063
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LMGYALLGFALCESVALFRLLVTFLILFG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=22
/product="ATP synthase F0 subunit 9"
                                                                                 anticodon=(pos:8676. .8678,aa:Leu)
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9562. .9633
gene="trnF(gaa)"
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                                                                                                                                                                                                                                                                                 .8784, aa:Pro)
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/product="tRNA-Ser"
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                                'gene="trnL(cag)"
'product="tRNA-Leu"
                                                                                                                                                                                                                                                       product-"tRNA-Pro"
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8749. 8821
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'gene="trnP(ugg)"
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                                                                                                                                                                                                                                                                                                                 1749. .8821
/gene="trnP(ugg)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9643. .9714
/gene="trnE(uuc)"
9767. .10804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="orf345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="orf345"
/9767. 10004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9767. .10804
/gene="orf345"
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                                                                                                                                                                                                                                                                                                                                                                            1867. .9088
'gene="atp9"
                                                                                                                                                                                                                                                                                                                                                                                                                                         8867. .9088
/gene="atp9"
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85; Conserv
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LOCUS
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10379. 10384
/note="predicted donor sequence, cag/gtaaaa, for exon 11 of MALAP2.03"
10541. 10550
/note="predicted splice acceptor sequence for exon 12 of MALAP2.03"
10707. 10712
/note="predicted splice donor sequence, tat/gtatgt, for exon 12 of MALAP2.03"
10766. 10775
/note="predicted splice acceptor sequence for exon 13 of MALAP2.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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11727. 11794,11978. 12324))
/gene="MALAP2.04"
                                                                                                                                                                                                                                                                                                                                                                                                                     'note="alternative splice acceptor sequence for exon 9 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALAP2.03"

10019. 10024

/note="predicted splice donor sequence, cac/gtaaga, for exon 9 of Malap2.03"

10160. 10169

/note="predicted splice acceptor sequence for exon 10 of forte" predicted splice acceptor sequence for exon 10 of forter forter for exon 10 of forter for
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10251. .10256
/note="predicted splice donor sequence, aag/gtaata, for exon 10 of MALAP2.03"
10330. .10339
/note="predicted splice acceptor sequence for exon 11 of MALAP2.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8589. 8594
/note="predicted splice donor sequence, tat/gtatat, for exon 7 of MAL4P2.03"
8628 . 8637
/note="predicted splice acceptor sequence for exon 8 of MAL4P2.03"
                                                                                                                                                                                                                                              9610. .9615
/note='predicted splice donor sequence, acc/gtaaat, for exon 8 of MAL4P2.03"
9645. .9650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9730. .9739
/note="predicted splice acceptor sequence for exon 9 f
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Pred. No. 0.22;
0; Mismatches 50; Indels 0;
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/gene="MAL4P2.03"
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Best Local Similarity 61.2%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAL4P2.03"
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|Db 222675 AGCAAAAA 222667
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                 misc_feature
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AC023268/c
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                                                                                                                                                           Alternative Steed (att/gtatga) for alternative donor sequence (att/gtatga) for alternative donor sequence (att/gtatga) for alternative Steeds for MAL4P2.03 fold (6794 . 6857,6942 . 7075,7272 . 7383,7566 . 7663, 7792 . 8064,8151 . 8357,8454 . 8588,8638 . 9609,9740 . 100170 . 10250,10340 . 10378,10551 . 10706,10776 . 10776 . 10787 ) fgene **MAL4P2.03 * 10176 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578 . 10578
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     /translation="myrnikyyfltnwkrtyrhysrkqninnlsnkikdpysdlykss
mygnnfkilpnkktksreyeiiktsnntysytspyppninytltppypesskkwyjenr
kyimkyknveyipikrltyknaskktnwntyyirmek"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-*hypothetical protein"
/protein_id-"CAB62844.1"
/db_xref-*cI:6562705"
/db_xref-*cPTREMBL:QUUL9"
/db_xref-*cPTREMBL:QUUL9"
/translation-*MNVEDRYKLIKEKYKEIKEQNDILKKAIIEYKKDLKELEKKNDI
LSNDKNQLQKNLTQLTNSLEEQKKKNSGWTNLMLLTKNSRENIHKSVAFEELEMKIKE
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MNTLHDLIVSLEKQINKINSEKNVNKFFIMCSICSNKNNIGRKYNPTCNMLYGLF"
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/note="predicted splice acceptor sequence for exon 2 of
MAL4P2.03"
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/note="predicted splice donor sequence, caa/gtaaat, for exon 2 of MAL4P2.03"
7262...7271
/note="predicted splice acceptor sequence for exon 3 of MAL4P2.03"
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/note="predicted splice acceptor sequence for exon 4 of
MAL4P2.03"
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/note="predicted splice acceptor sequence for exon 6 of
MAL4P2.03"
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//note="predicted splice donor sequence, atg/gtaata, for
exon lof MAL4P2.03"
6932. 6941
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//note="potential splice donor sequence, atg/gtaaaa, for
exon 3 of WAL4P2.03"
7556. .7568
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/note="predicted splice donor sequence, aac/gtttgt, for
exon 4 of MAL4P2.03"
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/note="potential splice donor sequence, caa/gtaaaa, for
exon 5 of MAL4P2.03"
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101292 11055.

101292 110489: gap of

110390 120867: contig of 10378 up.

120868 120967: gap of

131988: contig of 1018 bp in length

100 bp
                    9519 9618; gap of 100 bp 9619 13289 13388; gap of 100 bp 13389 13389; gap of 100 bp 13389 15599; contig of 2211 bp in length 15600 15699; gap of 100 bp 15700 21304; contig of 5605 bp in length 21305 21404; gap of 100 bp 2405 26070; contig of 4666 bp in length 26071 26170; gap of 100 bp 26071 26170; gap of 100 bp 26171 33773; contig of 5603 bp in length 26171 33773; contig of 5603 bp in length
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contig of 6959 bp in length
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     9518: contig of 2853 bp in length
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43487: contig of 5363 bp in length
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1. 2173
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15700. .21304
/note="assembly_fragment"
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/note="assembly_fragment"
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4420. .6565
/note="assembly_fragment"
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/note="assembly_fragment"
9619. .13288
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13389. .15599
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
/chromosome="9"
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56108: cont.
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Limmer, A. and Zody, M., Land, M., Charles Street, Cambridge, MA 02141, USA

Namitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 144457)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 9, clone RPl1-168D21
                         clone RP11-168D21 map 9, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13: M7815; 100% of reads Sequencing vector: M13: M7815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 133287 bases at least Q40 Consensus quality: 139023 bases at least Q30 Consensus quality: 141009 bases at least Q30 Insert size: 163000; agarose-fp Insert size: 142357; aum-of-contigs Quality coverage: 3.9 in Q20 bases; sum-of-contigs Quality coverage: 4.5 in Q20 bases; sum-of-contigs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

us-08-894-356c-1.rst

3	For clone info: please contact Research Genetics, Libraries Division tell 1-800-711-6195, email cdna@resgen.com Seq primer: Mi3F-R. Location/Qualifiers 1. 763 Source /organism="Solanum tuberosum" /cultiv@ir="Kennebec" /db_xref="taxon:4113" /clone="BBDLIOA14" /clone="BBDLIOA14" /tissue_type="lasf" /dev_stage="6 week old"	/note—"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Xho1; Whole plants were challenged with 450,000 Sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato. [156 g 233 t	tch 31 Similari 382; Cons GAGTATCGCT [GAGGTGACACT TCCCTTCTGTT	OY 198 AATCTTAAGGCCTCTTTGTCTCCTCTAAAACACTACGGTTAGGGGAAATTTG 257	CIGCTAGATCCATGATTTTTTTTTTTTTTTTTTTTTTTTT
SUMMARIES Result Ouery No. Score Match Length DB ID Description	141.2 8.3 763 155 86591758 141 8.3 575 142 86591758 127 7.5 690 155 86599447 122.8 7.2 591 167 86434257 119.6 7.0 564 142 86232746 111.4 6.5 508 173 86097054 111.4 6.5 578 143 8F051101 109.8 6.4 606 113 AW221049 107.8 6.3 570 142 8622784 107.6 6.3 603 118 AW31619	12 107.2 6.3 542 167 BR436185 14 101.6 6.0 659 155 BR598154 15 102.8 6.0 659 155 BR598154 16 5.4 5.7 549 21 Ar490445 17 93.6 5.5 687 111 Art20336 19 91.6 5.4 404 120 Art37239 20 90.8 5.3 518 119 Art650650 21 89.4 5.2 783 155 BG584708 22 87.4 5.1 414 142 BB521378 23 86.6 5.1 414 142 BB521378 24 5.0 5.0 6 5.0 5.26 105 Art386584	C 25 85.2 5.0 705 114 AW299055 AW299055 EST305729 26 84.6 5.0 788 114 AW299055 BW22180 BEST305729 28 82.8 4.9 487 118 AW516206 BW521804 EST307245 29 81.4 4.8 368 142 BE921953 BW521804 EST307245 31 78.4 4.6 648 154 BG521953 BW521951 EST307245 32 76.6 4.5 386 173 BG03769 BG037680 EST405720 33 75.6 4.4 505 154 BG50863 BG50863 Sac75609. 35 75.6 4.4 505 155 BG50863 BG50864 BG50863 Sac75609. 36 75 4.4 605 30 AV440958 AV440958 AV440958 37 74.6 4.4 605 30 AV440958 AV440958 AV440958 38 74.2 4.4 605 30 AV440958 AV440958 AV440958 AV440958 39 74 4.3 144 BF006679 BESTA00516	73.8 4.3 468 167 BE461227 73 4.3 403 143 BF052576 70.2 4.1 485 105 AL386583 69.8 4.1 569 119 AW719572 68 4.0 561 121 AW831571	RESULT 1 BG591758 LCCUS BG591758 CLCCUS DEFINITION EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone DEFINITION EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone ACCESSION BG591758 BG591758.1 GI:13609898 KEYWORDS SOLATO CORGANISM ENABLYOTE: VIIIGHDIANTAGE: Streptophyta; Embryophyta; Tracheophyta; Solanum tuberosum ENABLATIONS: Core eudicots; Asteridae: euasterids I; Solanales; Solanaceae; Solanum. Asteridae: euasterids I; Solanales; Solanaceae; Solanum. Asteridae: euasterids I; Solanales; Solanaceae; Solanum. Asteridae: Hornandez.M., Tornqvist.CE, Wirtz,U., Loukoianov.A., Rangel,P., Haberlach,G.T., Cho.J., Chiemingo,A., Bougri,O., Buell C.R., Ronning,C.M., Helgeson,J. and Baker,B.

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123 ATGTGCTGGAGATTTTAGAGCACGATTCAATCCACCACTCCTCAATCTTATGGGAA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 575)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                                                                                                                               BE920468 575 bp mRNA EST 02-0CT-2000 ST1412137 potato leaves and petioles Solanum tuberosum cDNA clone CSTB6C8 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
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/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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58.4%; Pred. No. 9.2e-27
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/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
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Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 690)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougrilo,, Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Unpublished (2000)
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EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
                                                                                                        1070 GCTTCTTGTTGCAGTTGCAGCTATTGGAGAGCCATTGAAAAGAGGTTGCACAACGAAAA 1129
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                            1013 CTGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGG
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/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
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/cultivar="Kennebec"
/db_xxef="taxon:4113"
/clone="GSTS5122"
/clone_lib="cSTS"
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Tel: 864 656 4366
Fax: 864 656 4293
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                     4 AATGTCAAGTTGCGCCACCTCCGGGGGGGCA---GCGGAGGTGACACTCCCTCTTACTT
                                                                                                                              TCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACGACTTTC
                                                                                                                                                          61 ATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTACAAGCTCC
                                                                                                                                                                                                       AGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCCAATGATTTGC
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                Length 690;
               7.5%; Score 127; DB 155;
llarity 52.9%; Pred. No. 5.1e-23;
Conservative 0; Mismatches 315;
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clone cLEG15H6, mRNA sequence.
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/note-vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 297 491 357 551 417 611 477 671 537 AACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTACGTTA-----TGTGACA 180 CATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATA 431 132 ATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTT 191 99 AATTTGTTGATGCCGATCANATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAG AACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTT GGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGT 241 GACCATCGCGTAAGGCTAAGGATTTTTAT---CACTTTGTTCCTAAGTTAGGGGAACCT AGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCT GTAATGTTCATCAAGCCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTG TCCGCGAATCTTCTTCCATCTTTCGATAGATCGATAAATCAAAGATCTGTATGGCCTAGAG stage 7.2%; Score 122.8; DB 167; Length 591; llarity 53.7%; Pred. No. 6.5e-22; Conservative 0; Mismatches 252; Indels 9; breaker fruit, TIGR' tomato fruit tissue, esculentum" USA /organism="Lycopersicon escul /cultivar="TA496" /db_xref="taxon:4081" /clone="cLEG1546" /clone=lib="tomato breaker fr /tissue_type="Pericarp" /dev_stage="breaker" Unpublished (2000) Contact: David Frisch Clemson University Genomics Institute Clemson University 29634,

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DEFINITION
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                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Aspernatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 574)
van der Hoeven, R. S., Bezzerides, J., Holt, I. E., Liang, F., Cho, J., Van der Hoeven, R. S., Bazzerides, J., Bougri, O., Buell, C. R., Ronning, C. M., Fry, Ww. E., Tanksley, S. D. and Baker, B.
Generation of Ests from potato leaves and petioles
                                      BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTE21112 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 121; DB 142;
Pred. No. 1.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 9
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123 c 106
                                                                                                                    BE922746.1 GI:10448822
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                                                                                                                                                                               Solanum tuberosum
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                                                                                                                                                             potato.
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                                                                                                                      VERSION
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                    BE922746
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/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cho, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Steridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 564)
van der Hoeven, R. S., Bezzerides, J., Holt, I. E., Liang, F., Cho, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE921494 564 bp mRNA EST 02-OCT-2000
EST425179 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                     Contact: Cathy Rouning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
490 CTAACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTT 549
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                                  610 TGTCCGCGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liang, F., Ch
Buell, C.R.,
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                                                                                                                      550 TTGTAATGTTCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGT
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/organism="Solanum tuberosum"
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db.tref="taxon:4113"
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/clone_1b="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lbb_host="SOLR"
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Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Bue
, C.M., Fry, M.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
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53.8%; Pred. No. 4.6e-21;
Live 0; Mismatches 244; Indels
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Best Local Similarity
Matches 298; Conserv
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                                                 Query Match
Best Local Si
Matches 276;
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ORGANISM
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/cultivar="Kennebec"
/db_rare="Exaxon:4113"
/clone="csrab45p9"
/clone=lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/tissue_ge="B weeks old plants"
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/note="Wector: pBlueScript SK(-); Fite_1: EcoRl; Fite_2: EcoRl;
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Solanum tuberosum
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases I to 508)
Van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Unpublished (2000)
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EST461573 potato leaves and peticles Solanum tuberosum cDNA clone
CSTB45P9 5' sequence, mRNA sequence.
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CGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGGACTCGATAACTTTGATCG
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The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 TCTCCCTCACTCTCAAACACTACACACCCTTAGCTGGCAACATTGCTTGTCCACTAAATT
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                                                                          TGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAAT
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Makaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,R.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AGTGGTTATCCTGAGTTGCGTTA-----TGTGACTGGAGATTCTATATCTGTTACTTTT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 TIGCATGGCCTTTTTTTTTTTTTTGCCACGGGTTATAAGGACCATGCAAGACTATAAAGTG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 TTTTATCCCTTCATTCCTCAATTGGCACAACCTAAGGATGCACCGGGGGTC---AAACTA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTAAGGCCTCTTTG 215
                                                                                                                                                                                                                                                                                                                                                                                   276 GGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAACTTTGATCGTT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 GCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAACTGGTAGATTCCAATGAT 395
                                                                                                                                                                                                                                96 ACATICITCGATATCCCCIGGTIGCACTIGAATAAGAIGCAGICCCITCTGTTTTACGAC 155
                                                                                                                                                                                                                                                                                       62 ACTTATTTTGATCATATNIGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAG 121
                                                                                                                                                   BF051101 578 bp mRNA EST 16-OCT-2000 EST436276 tomato developing/immature green fruit Lycopersicon esculentum cDNA clone cLEM21H7 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation of ESTs from tomato fruit tissue, immature green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 TCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAATGG
                                                                                                                 36 GAAAAATGCCAAGTTACACCACCATCTGACACAAAAGATGTCGAGTTATCGCTACCGGTA
Length 508;
                                                          Indels
DB 173;
Score 111.4; DB 173,
Pred. No. 6.8e-19;
0; Mismatches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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Contact: David Frisch
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 ACGCACATCATTCAATTCCAGATGCTAAAA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 AGTAACCATCATGTCGCTTGTGATGGAAATA 503
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Location/Qualifiers
1. .578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:10804997
6.5%;
llarity 54.0%;
Conservative
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321;
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ORIGIN
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                                                                                                         JOURNAL
COMMENT
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                                         REFERENCE
                                                    AUTHORS
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                                                                                           TITLE
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                                                                                                       /note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masses of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW221049 606 bp mRNA EST 07-DEC-1999 SET297518 tomato fruit mature green, TAMU Lycopersicon esculentum CDNA clone cLEF3F1, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1014 TGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTACAGCGGATTGCCGAGGACTTCTGACGCCCCGTGTCCGCCTAACTACTTTGGCAAC 1013
                                                                 /tissue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AGAGGACGCGATAGGAGAGAGATGATCATAGATGATGTTAGTATCGGA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAACCCCCTCGATTCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCTGAAATC 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   953
                                                                                                                                                                                                                                                                               546 AGTTTTGTAATGTTCATCATGCTTGGGCCTATATTAACAATTTGGGAAAGACGCGGAC 605
                                                                                                                                                                                                                                                                                                                                                   CTAGAGGAAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTTGGA 725
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                           64
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/culd_xref="cultivar="0.401"
/clone="c.LEM2147"
/clone_lib="tomato developing/immature green fruit"
                                                                                                                                                                                                                                                                                                                                                                                                       5 ACTATAGCAGGGTTCATTAAGGCGTGGGCTCTACTCCACAAATTCGGTGGACATGAACAA
                                                                                                                                                                                                                                                                                                                                     TTGTTGTCCCCCGAATCTTCCTTCCATCTTTCGATAGATCGATAAATCAAAGATCTGTATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  894 AAAGATGACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAAGCTAAAGAACAAAGTACTGAATCTCAGAGGATCCG------AACCGACA
                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                             578;
                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                            Score 111.4; DB 143; Lengtl
Pred. No. 7e-19;
0; Mismatches 241; Indels
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                                                                                                                                                                                                                            6.5%;
                                                                                                                                                                                                                                                     Matches 317; Conservative
                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                        192
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                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                       BASE COUNT
ORIGIN
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Opton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue Unpublished (1999)

Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds were discarded prior to freezing the pericarp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TGATA---CTCCCTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 CCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GGATATTTTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 TGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAAC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGTGTCTGTTACTTTTTTCGAGACTGATATGAATTTCAATTATCTCATTGGTGACCATC 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 AGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .606
//organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="clEF3F1"
/clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 ATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                               100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4586
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang, F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley,S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Būkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 24-MAR-2000

> Cornell University Lycopersicon

, mRNA sequence.
                                                                                                                                                                                                        355
                                                                                                                                                                                                                                                                                               412
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/tissue_type="trichome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTC
                                                                                                                                                           302 CCGTGATGAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTA
                                                                                                                                                                                                     299 ---TGTGACAGGAGATTCTGTATCTGTTACTTTTTCTGAGACTGATATGGATTTCAATTA
                                                                                                                                                                                                                                                       362 CCTTAAAGGTCATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCC
                                                                                                                                                                                                                                                                              356 TCTCATTGGTGACCATCCGCGTAATGCTAAGGATTTTTAT---CACTTTGTTCCTACGTT
                                                                                                                                                                                                                                                                                                                                                                     482 CGTTTTTCCTAACCGTGGCATAGCCGTGGCTCTGACGCCACATCATTGCAGATGC
                                                                                                              242 CTTAGCTGGAAACGTTGCTCGTCCACTAGATACAAACGGATATCCTGAGTTACATTA---
                                                                                                                                                                                                                                                                                                                                              422 ACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon hirsutum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: David Frisch
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Email: dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW616119 603 bp mRNA
EST296884 L. hirsutum trichome,
hirsutum cDNA clone cLHT6C7 3',
AW616119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 TAAAAGTTTTGTAATGTTCATCAATGCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:62890"
/clone="cLHT6C7"
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1. .603
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1 (bases 1 to 6C3)
van der Hoeven, R.S.,
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KEYWORDS
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El (bases 1 to 570)

Strate Hoeven, R.S., Bezzeridaes, J., Holt, I.E., Lianag, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of Ests from potato leaves and petioles
Unpublished (2000)

Contact: Cathy Ronning
The Institute for Genomic Research
For Clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                   potato leaves and petioles Solanum tuberosum cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GGACACTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.3%; Score 107.8; DB 142; Length 570; Best Local Similarity 53.1%; Pred. No. 6.3e-18; Matches 304; Conservative 0; Mismatches 257; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACGCGGACTTGTTGTCCGCGA
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499 GCATAGCCGTGGCTCTGACGCCACATCCATTGCAGATGCTAAAAGTTTTGTAATGT
                            // Solutivariantels
// Organism="Solanum tuberosum"
// Cultivar="Kennebec"
// Cultivar="Kennebec"
// Conne_1b="Express"
// Clone_1b="potato leaves and petioles"
// Close_1b="potato leaves and petioles"
// Close_1b="potato leaves and petioles"
// Close_1b="solato leaves and petioles"
// Close_1b="Solato leaves old plants"
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CSTB32E2 5' sequence, mRNA sequence.
BE922784.1 GI:10448860
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ORIGIN
                                                                                       259
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AUTHORS
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KEYWORDS
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/clone_lib="tomato breaker fruit, TIGR
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BG598154
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 542)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE436185 542 bp mRNA EST 24-JUL-2000 EST407263 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG31A19, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              1260 AAATTTGACATTACCTC----TGTTGATTATGCAGAATTGATTTATGTGATTCAG 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGAT 1370
                                                                        GATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCG 1022
                                                                                                                                   1023 TCATGCGTTGCAAAAGCAACA---CATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTT 1079
                                                                                                                                                                                                                                                                                                                  1200 ATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCA 1259
                                                                                                                                                                  483
                                                                                                                                                                                                                                                                                      422 AATGGTG-----ATTGGTTAAAAGTATTAGACAACATAGATGTGATTGGATCATTTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTT
                                                                                                                                                                                                                                                        1140 GCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation of ESTs from tomato fruit tissue, breaker stage
            Length 603;
                                            18;
                         (.3e-18;
nes 179; Indels
              DB 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
           Score 107.6; I
Pred. No. 7.3e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"taxon:4081"
/clone-"cLEG31A19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE436185.1 GI:9434028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: David Frisch
           6.3%;
ilarity 57.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 4366
Fax: 864 656 4293
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                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tomato
                                         263;
              Query Match
                               Local
                            Best Loca
Matches
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DEFINITION
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

70 c 132 g 165 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1013 CTGTCTTGCGTCATGCGTTGCAAAAGCAACA---CATAAAGGTTAGTTGGGGATAAAGG 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ATGTGCAGCAGATTTTAGAGCGCGATTCAATCCACCTTCCTCAATCTTATTTTGGGAA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AGAGGACGCGATAGGAGAGAGATGATCATAGATGATAGTGTAATGGAATGTTTCGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chiemingo, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Rouning
the Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
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1 (bases 1 to 659)

van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 TTGCATAGTTGGGTATGTCACAAAATCAATAAGGCATGTTGATTAGTTGGAAGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 ATGGGTCCTTAATGGTG-----ATTGGTTAAAAGTATACGACAATGTAGATGTGATTCG
                                                                                                                                                                                                                                                                                                                                                                        542;
                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                     Score 107.2; DB 167; Lengt
Pred. No. 9e-18;
0; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1250 AAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGA 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Pericarp'
                         /dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG598154.1 GI:13616294
                                                                                                                                                                                                                                                                                                                                                                        6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.7
Matches 262; Conservative
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1 (bases 1 to 497)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannon1,J. Generation of ESTs from tomato fruit tissue
Unpublished (1999)
Contact: David Frisch
                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 TCTTTGTCTCTCACTCTAANACACTACGTTCCGCTTAGCGGAAATTTGTTGTTGTGCGATC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GATACAAACGGATATCCTGAGTTACGTTA-----TGTGACAGAGATTCTGTGTCTGTT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 AATGATITGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCATGCAAGACTAT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AAGGATTTTTATCACTTTGTTCC---TAAGTTAGGGGAACCTAAGGATGCACCGGGGGTC 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 AAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAACTTTG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 CAACTAGCCCCGCTCTTAGCCATTCAGGTGACACTTTTTCCGAATCTTGGTGTATCCATT 292
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%; Score 101.6; DB 122; Length 497; Best Local Similarity 54.0%; Pred. No. 2.7e-16; Matches 256; Conservative 0; Mismatches 209; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
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/clone_lib="tomato fruit mature green, TAMU"
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es 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .497
/organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                              100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366 Fax: 864 656 4293 Emall: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
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                          Lycopersicon esculentum
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COMMENT
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                                                                                              /clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11b="cSIV"
/clone_11be="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_lost="SOLR"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers:
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AW930934 GI:8106335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTITIATCCCTTCATTCCTCAATTGGCACAACCTAAGGATGCACCGGGGGTC---AAAC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCATAGCCGT----GG 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 TTGAGCAATGCCAAGTTGCGCCACCTCCCCACGGCGCGCAACAGAGCTAACGCTCCCTC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 TAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGTCCCTTCTGTTTTACG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCAC 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 102.8; DB 155; Length 659;
Pred. No. 1.4e-16;
0; Mismatches 257; Indels 13; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 TTGAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCGAGTTATCGCTACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 ACTITCCGTACCCAAGAACACATITCTTGGACACTGTTATCCCTAATCTTAAGGCCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 TGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGCCGATCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACTCGATAACTTTGATCG
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                                                    /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                           206
                                                                         /cultivar="Kennebec"
/db_xref="taxon:4113"
Location/Qualifiers
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Best Local Similarity 53.4%;
Matches 310; Conservative (
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                             AW221050 583 bp mRNA EST 07-DEC-1999
EST297519 tomato fruit mature green, TAMU Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 ATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 CICTTAAAAATTCACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCCGGAAACGTTG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 AGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGCACTTGAATAAGATGCAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 CCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 TGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCGACT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AAATGGTGAAGGTTCTTGAAAAATGCCAAGTTACACCACCATCTGACACAACAGATGTCG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ACATGGCCACCGTGATTGAGCAATGTCAAGTTGCGCCACCTCCCGGCGGCGCAACGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
Score 101; DB 113; Length 583;
Pred. No. 4.1e-16;
0; Mismatches 260; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .583
/organism="Lycopersicon esculentum"
/cultivar="14496"
/db xref="taxon:4081"
/clone="cLEF3F3"
/clone lib="tomato, fruit mature green, TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Fax: 864 656 4293 Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                     CDNA clone cLEF3F3, mRNA sequence.
AW221050
AW221050.1 GI:6532734
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                                                                                                                                                                                                                                                                              Lycopersicon esculentum
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                                                                                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                 DEFINITION
                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                    AW221050
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                                                                                     RESULT
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CGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAAC 378
                                                                                                                                                 CTGTGTCTGTTACTTTTTCGAGACTGATATGAATTTCAATTATCTCATTGGTGACCATC 352
                                                                                                                                                                                                               379 TGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTTATAAGGACCA 438
                                                                                                                                                                                                                                                                            353 CGCGTAAGGCTAAGGATTTTTAT---CACTTTGTTCCTAAGTTAGGGGAACCTAAGGATG 409
                                                                                                                                                                                                                                                                                                                                       439 TGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTG 498
                                                                                                                                                                                                                                                                                                                                                                       GCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGT 558
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Appli Appli

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1603 TGTTACGATAGGTATTGTATMATGCCATTATATACTTCCATAAAGTATCCTATGCAATAG 1662
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Sequence 35,
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APPLICANT: Cokazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Kawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amann, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF MEXI EXPRESSION
FILE REPRENCE: RTS-1016
CURRENT APPLICATION UNBER: US/09/197,380
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.8; DB 3; Length 2
Pred. No. 0.022;
0; Mismatches 37; Indels
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US-09-031-485-1

US-09-031-485-3

US-08-847-429A-1

US-08-847-429A-3

US-09-065-474-3

US-09-031-485-6

US-09-031-485-8

US-09-031-485-8

US-09-031-485-8

US-09-031-485-8

US-09-031-485-8

US-09-065-474-6

US-09-065-474-8

US-09-065-474-8

US-09-031-485-35

US-09-031-485-35

US-09-031-485-35

US-09-031-485-35

US-09-031-485-36

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US-09-031-485-36
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; Sequence 1, Application US/03738349
; Patent No. 5869538
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence I, Application US/09197380; Patent No. 6096543; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%;
Best Local Similarity 63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Conservative
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US-09-197-380-1
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US-09-197-380-1
       SEQ ID NO 1
LENGTH: 23
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Sequence 10, Appl
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Sequence 9, Appli
Sequence 10, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 10, Al
Sequence 102,
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                                                                                                                                                                     ; Search time 168.74 Seconds
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Sequence 1, P
Sequence 1, P
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Sequence 5, 1
Sequence 4, 1
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Sequence 2,
Sequence 9,
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Sequence 5,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd
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US-09-065-474-103
US-09-031-485-9
US-09-031-485-10
US-08-847-429A-9
US-08-847-429A-10
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US-09-065-474-146
US-09-031-485-4
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US-09-065-474-4
US-09-065-474-5
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-08-684-862-10
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US-08-021-608D-9
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US-08-726-160-1
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US-08-821-994-64
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                               GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                   5, 2001, 13:53:20
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1703
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Maximum DB seq length: 2000000000
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Match Length
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1585 ACCTCACACCTGACATGGTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATA 1644
                                                                                                                           7003 acattatactttataactaatagataacagttttttacatattaaatatgttctacttaa 7062
                                                                                                                                                                 DB 4; Length 7122,
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DÜNCAN,
APPLICANT: LEVENS, DAVID L., DÜNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
         Score 39; DB 4;
Pred. No. 0.24;
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S FEILER
REGIGENATION NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-689
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08021608D Patent No. 5580760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
         2.3%;
58.0%;
Query Match
Best Local Similarity 58.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILLING DATE: 22-FEB-19-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-021-608D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unknown
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
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                                                                                                                                                                                                                                                                            US-08-021-608D-9
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| Patent No. 6210950
| APPLICANT: Johnson, William G. APPLICANT: Stenroos, Edward S. TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
| TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
| FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Indels
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Score 39.8; DB 2;
1larity 79.7%; Pred. No. 0.1;
Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                        PRICE APPLICATION: 439
PRICATION NUMBER: US 08/364,439
FILING DATE: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BATEAT
REGISTRATION NUMBER: 32,013
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323-00000
TELECOMUNICATION INFORMATION:
TELECHOME: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 2
LENGTH: 7122
                         : 1300 I Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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284..2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-318-448-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
""+rhes 47; Conserva
           Dunner
         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
US-08-738-349-1
                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-318-448-2
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                                               CITY:
STATE:
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ö 1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675 Gaps ö Query Match 2.3%; Score 38.4; DB 1; Length 2381; Best Local Similarity 64.8%; Pred. No. 0.22; Matches 57; Conservative 0; Mismatches 31; Indels 0 470 bp variable region where R is A or G. δ

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Sequence 9, Application PC/TUS9401782
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 470 bp variable OTHER INFORMATION: region where R is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICTATION:
PLING DATE: 22-FEB-1994
CLASSIFICTATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
TILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 75-6480
TELEPHONE: (212) 75-6490
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
      2320 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY OISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2381
TYPE: Nucleic acid
TYPE: Nucleic acid
STRANDEDNESS: Double
TADOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEW YORK
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL TYPE:
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
                                                                                                  RESULT 6
PCT-US94-01782-9
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION
2260 AATGTATACATTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATGATGATGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2260 AATGTATACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATAGAAACC 2319
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                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08726160
Patent No. 5734016
GENERAL INFORMATION
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 bp variable region where R is A or G.
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CALT: 10154
MEDIUM TYPE: FLOPPY DISK
COMPUTER: TBM FC COMPATIBLE
COMPUTER: TBM FC COMPATIBLE
CORPATIBLE
COMPUTER: TBM FC COMPATIBLE
CORPATIBLE
CORPATIBLE
CORPATIBLE
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CORPATIBLE
CORPATIBLE
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-0CT-1996
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 2026-4063US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEMENTICE
COMPUTER: CALCES
COMPUTER:
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                                                                                               1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                                                                2320 TCAAAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2381
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 64.8
Matches 57; Conservative
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COTHER INFORMATION:
US-08-726-160-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW Y STATE: NEW COUNTRY: US ZIP: 10154
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Length 2381;

Score 38.4; DB 5; Pred. No. 0.22;

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2323 TCAAAAAAAAAAAAAAAAAAAAAAA 2350
                      1676 TGTTAAAAAAAAAAAAAAAAAAAAA 1703
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Best Local Similarity 64.83
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Un
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       10154
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                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                       RESULT 8
US-08-726-160-1
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                                       1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAAACATGTTATG 1675
                                                                            2260 AATGTATACTTTCACTTTCCAAATGCCTGTTTTGTGCTTTACAATAAATGATATGAAACC 2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
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    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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  31; Indels
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variable region where R is A or G.
                                                                                                                                                                                                                                                    Sequence 1, Application US/08021608D

Patent No. 5580760

GRMERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 38.4; DB 1;
64.8%; Pred. No. 0.22;
tive 0; Mismatches 31;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SOFTWARE:
SOFTWARE:
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 25-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION OF A:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2056-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 758-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                   1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                                                            2320 TCAAAAAAAAAAAAAAAAAAAAAAA 2347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ): 345 PARK AVENUE
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3'
Best Local Similarity 64.8'
Matches 57; Conservative
57; Conservative
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STRANDEDNESS: Doub
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OTHER INFORMATION:
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ORIGINAL SOURCE:
ORGANISM: Human
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEW YORK
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MOLECULE TYPE:
HYPOTHETICAL: N
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  Matches
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tive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 bp
variable region where R is A or G.
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVICAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1676 TGTTAAAAAAAAAAAAAAAAAAAAAAAA 1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 04-0CT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/021,608
FILING DATE: 22-FEB:1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION UNDRER: 26,728
REPRENCE/DOCKET UNDRER: 2026-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
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1616 ATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATG 1675
                           2263 AATGTATACTTTCCAAATGCCTGTTTGTGCTTTACAATAAATGATAGAAACC 2322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1602 GTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATA 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bach, Alfred
APPLICANT: Hillen, Heinz
APPLICANT: Hillen, Heinz
APPLICANT: Hillen, Heinz
APPLICANT: Bialojan, Siegfried
TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kell 6 Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage.
COMPUTER: Diskette, 5.25 inch, 360 Kb storage.
COMPUTER: DISKETTE, MS-DOS VERSION 5.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
PELLING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 4;
Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                                                                                          FALLEN UNFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
TTLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
SALIER FILING DATE: 1997-03-18
                                                                                           1676 TGTTAAAAAAAAAAAAAAAAAAAAAAA 1703
                                                                                                                  2323 TCAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2350
                                                                                                                                                                                                             RESULT 10
US-00-3811994-64
Sequence 64, Application US/08821994A
; Patent No. 6228643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Brassica napus
US-08-821-994-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.C.
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-684-862-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                          qq
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                                                                                                        APPLICANT: THE GOVERNMENT OF THE UNITED STATES
APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: 473 bp
OTHER INFORMATION: variable region where R is A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATE:

TILING DATE: 22-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728

REGISTRATION NUMBER: 26,728

REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800

TELEPHONE: (212) 758-689

INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
LEMGTH: 2384

LEMGTH: 2384

LEMGTH: 2384

TYPE: Nucleic acid
STRANDEDNESS: Double
TYPE: Unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: 22-FEB-1994
                                                              Sequence 1, Application PC/TUS9401782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANELLE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE: HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
              RESULT 9
PCT-US94-01782-1
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Gaps

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1042 CACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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                                                                                                                                                                                                                                                                                                                    26 CACAAGAACCGTTTTTCAGCAAGTAGGCTATAATGGGACACCTGGAGATCCAGAAGAAC 85
                                                                                                                                                                                                                                                                                                                                                                                 1102 CCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                          86 CCAAAGAACAGTCATTCCACGAAGAGGAAGAGGAAGTTGCAGTTTCAGAAATTCG 140
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                                                                                                                                                                                                            DB 3; Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 36.6; DB 3;
57.4%; Pred. No. 0.21;
tive 0; Mismatches 49;
                                                                                                                                                                                                       2.1%; Score 36.6; DB ilarity 57.4%; Pred. No. 0.21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Carol Talkington Verser, Ph.D. STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 =
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24-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 103, Application US/09065474 Patent No. 6063599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 103:
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LENGTH: 184 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.18
Best Local Similarity 57.45
Matches 66; Conservative
         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                     1..183
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2. CLASSIFICATION:
                                                                                               NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: 1i
; MOLECULE TYPE:
US-09-065-474-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-065-474-103/C
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                                                                                                                                        US-09-065-474-102
                                                                                                                   LOCATION:
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Patent No. 6063599

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tang, Liang

APPLICANT: Blehm, E. Scot

TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 171

CORRESPONDENCE ADDRESS:

ADDRESSEE: Garol Talkington Verser, Ph.D.

ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive

CIVITY: Fort Collins

STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 197 to 904

CTHER INFORMATION: the coding region shown in (2)(ix)(B)

CTHER INFORMATION: codes for the protein of SEQ ID NO: 5
US-08-684-862-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 2.2%; Score 37.2; DB 1; Length 9 Best Local Similarity 77.6%; Pred. No. 0.31; Matches 45; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordberfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24-APR-1998
CLASSIFICATION:
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Veresr, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHONE: 970/494-9505
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERIZIUS:
LENGTH: 184 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    CDNA to mRNA
                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                           TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
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Search completed: November 5, 2001, 18:03:41
Job time: 15021 sec
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159 CAÇAAGAACCGTTTTTCAGCAAGTAGGGTATAATGGGACACCTGGAGATCCAGAAGAAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 CACAAGAACCGTTTTTCAGCAAGTAGGGTATAATGGGACACCTGGAGATCCAGAAGAAC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                             1102 CCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 CCAAAGAACAGTCATTCCACGAAGAGGAAGAGGAAGTTGCAGTTTCAGAAATTCG 338
                                                                                                                                                                                                                                                                       APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DROFILIARIA, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESSEE: Ground Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36.6; DB 1; Length 810;
Pred. No. 0.42;
0; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/031,485
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24 APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    Sequence 9, Application US/09031485 Patent No. 5824306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%;
Best Local Similarity 57.4%;
Matches 66; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 810 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80525
                                                                                                                                                                                                -09-031-485-9
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US-09-031-485-10/c ; Sequence 10, Application US/09031485 percent No. 5824306 ; GENERAL INFORMATION:

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1042 CACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATTGGAGAAG 1101
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  DIROFILARIA AND BRUGIA ANKYRIN
PROPEINS, NUCLEIC ACID MOLECULES, AND
USES THEREOF
85
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                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MADLUM TYPE: Floppy disk
MADLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WAINdows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,485
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/847,429
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
RELECOMMUNICATION NUMBER: 37,459
RELEPHONE: 970/493-7272
INFORMATION FOR SEO ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.1%; Score 36.6; DB 1;
Best Local Similarity 57.4%; Pred. No. 0.42;
Matches 66; Conservative 0; Mismatches 49;
                                                                    NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 810 nucleotides
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STRANDEDNESS: single
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; MOLECULE TYPE: CDNA
US-09-031-485-10
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                 USA
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Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
6..1415
7.tag- a
/product- Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                AAC66940
AAQ44311
AAX5265
AAX33336
AAX31100
AAF21920
AAF21920
AAF2167
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(SUNR ) SUNTORY LTD
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17-FEB-1995;
29-JUN-1995;
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2400.315 Million cell updates/sec
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                                                                                                                                                                                              November 5, 2001, 13:54:25 ; Search time 445.49 Seconds
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**Sidesty-Geneseq_Geneseq_NA1981_DAT:**

**Sidesty-Geneseq_Geneseq_NA1991_DAT:**

**Sidesty-Geneseq_Geneseq_Geneseq_NA1991_DAT:**

**Sidesty-Geneseq_Geneseq_Geneseq_NA1991_DAT:**

**Sidesty-Geneseq_Geneseq_Geneseq_NA1991_DAT:**

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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Nucleotide sequency
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Human c-myc far up
Human o-myc far up
Human o-myc far up

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Arabidopsis thalla Human colon cancer Human MEK1 DNA. H Human breast cance

Sequence:

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Searched:

Database

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Result è.

n colour Six plants Vectors containing DNA fragments encoding proteins of plant originate aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colotone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers Ξ Mizutani Ė Kusumi 94pp; Japanese Fukui Y, Yonekura Fujiwara Page 53-57; Tanaka Y, 1996-393401/39 P-PSDB; AAW04722 Ashikari Nakao M, Claim 4; NAME OF STREET AND ASSESSED BY A STREET BY A STR

T; 0 other; BP; 512 A; 353 C; 356 G; 482 Sequence 1703

ö 180 180 300 360 360 420 420 480 480 900 99 120 300 999 9 9 CTGACACAACAGATGTCGAGTTATCGCTACCGGTAACATTCTTCGATATCCCCTGGTTGC TGGACACTGTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTC CACGGGTTATAAGGACCATGCAAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAA **ACTTGAATAAGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCT** tggacactgttatccctaatcttaagccctctttgtctctcactctaaaaacactaccttc CGCTTAGCGGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACT CCCGTGATGAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACT ACCTTAAAGGTCATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGC CTAAAAGTTTTGTAATGTTCATCAATGCTTGGGCCTATATTAACAAATTTGGGAAAGACG ctaaaaagttttgtaatgttcatcaatgcttgggcctatattaacaaatttgggaaagacg CGGACTTGTTGTCCGCGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGT Length 1703; ö Indels DB 17; ÷, 99.7%; Score 1698.2; llarity 99.8%; Pred. No. 0; Conservative 0; Mismatches Best Local Similarity Matches 1700; Conserv Query Match Best Local 121 181 241 301 361 421 481 541 61 61 121 181 241 301 361 421 481 601 g ò g g à ò 9 9 ò Q G à ò QQ å Q à g 9 ò

961 CGGATTGCCGAGGACTTCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTG CAGATGCAAAAACTTGGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGA AATTTGACATTACCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCAGGGATT TTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAA ttgaaaaaaggtgtggagattggagtatcattgcctaagattcatatggatgcatttgcaa TTGGAAGCAAACCCCCTCGATTCAACAAGGTACGAGCTACATATGTCCTCTCCCTTGCTG ACGTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAG 1021 CGTCATGCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAAGGGCTTCTTGTTG CAGTTGCAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTG 1201 TTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTGCAA 1261 aatttgacattacctctgttgattatgcagaattgatttatgtgattcagtccagggatt AAATCTTTGAAGAAGGCTTTTGCTCTTTGTCATAGTCTCTTTAATAGAACCATATTTGCT 1441 GCAATAAAGTACCAAGTCCTTTAGTAACACTACAAACCCTACTTTCGAGGCGGGAAC ACCACAACGAGGTTCAATCACTAGAAGGTTGTACTTCATAAATTCCAGAGGTCGAATATA CACCGTTGTCCTCTGAAAGTTGAACCTCACACCTGACATGGTGTTACGATAGGTATTGT ATAATGCCATTATATACTTCCATAAAGTATCCTATGCAATAGAGAACATGTTATGTGTTA atggcctagaggaaacattttggaacgaaatgcaagatgttcttgaaatgttctctagat AAATCCAGAAGCTAAAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATACGTG 1141 1321 841 1201 1381 1561 1081 1261 1381 1501 1621 721 841 1321 1561 1681 1681 721 781 901 1621 δ g à q δ g ò 셤 δ g οy g δ Q ò 8 οy g QΥ g ð g οy g δ a δy g δy qq ò q ò a

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     aacaatctttatcggtcactcttcaacattttttcccgtttgctagtaatttgattgtat
                                      --- ATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGATGAGGGCG
                                                                                                         ACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATC
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                                                                      ttcctaacactgatggttcgggttttaataaaaaaccagaaataaaacacgttgaaggtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 TGAAGGTTCTTGAAAATGCCAAGTTACACCACCATCTGACACACAGATGTCGAGTTAT
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                                                                                                                                           anthocyanin pigment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                                                                                                                                      plants; acylation; colour; tone; colouration; colour change;
Gentiana triflora; Petunia hybrida; Perilla ocimoides;
Scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1508 BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                /*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                         Aromatic acyl transferase; transformation;
                                                                                                       Aromatic acyl transferase coding sequence.
   BP
 mRNA; 1508
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                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                             cruentus (Clone pCAT8).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     95JP-0046534.
95JP-0067159.
95JP-0196915.
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AAT37312 standard; cDNA to
                                                                   (first entry)
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Best Local Similarity 52.0%
Matches 720; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1995;
29-JUN-1995;
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                                    AAT37312
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AGATTGGAGTATCATTGCCTAAGATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAG 1395
                                 Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the fitower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAM7308-737313. NOTE: This sequence is supposed to cross reference with the protein described in AAW04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided not to cross reference the two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding for aromatic acyl transferase - for transforming plants the produce anthocyanin pigments and thus altering colour tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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/product= Aromatic acyl transferase.
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Nakao M, Tanaka Y, Yonekura K;
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                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                               AAT37313 standard; cDNA to mRNA; 1518
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Length 1518;

Score 193; DB 17; Pred. No. 6.3e-42;

11.3%; 51.2%;

Query Match Best Local Similarity

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                                                                     AAGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACT 188
                                                                                                                                                                                                               GGAAATTTGTTGATGCCGATCAAATCGGGCGAAATGCCGAAGTTTCAGTACTCCCGTGAT 308
                                                                                                                                                                                                                                               tgcaatctaatctaccctctatcgccggagaaatgccggagttccggta----tcag 275
                                                                                                                                                                                                                                                                                    GAGGGCGACTCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAA 368
                                                                                                                                                                                                                                                                                                      GGTCATCAACTGGTAGATTCCAATGATTTGCATGGCCTTTTTTATGTTATGCCACGGGTT 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| atagtogaggaatctgatoggaaattgtttcaagttttagcogtgcaagtgactctgttt 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTAACCGTGGCATAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGT 548
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                                acggtggctgagcagtcactcccgctcaccttcttcgacatgacgtggctgcatttccac 101
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                                                                                                                                           GTTATCCCTAATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGC
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                                                                                                                      1263 TTTGACATTACCTCTGTTGATTATGCAGAATT---GATTTATGTGATTCAGTCCAGGGAT
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containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                   25 TGAAGGTTCTTGAAAATGCCAAGTTACACCACCATCTGACACACAGATGTCGAGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 AAGACTATAAAGTGATCCCGCTCGTAGCCGTGCAAGTAACCGTTTTTCCTAACCGTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 TAGCCGTGGCTCTGACGGCACATCATTCAATTGCAGATGCTAAAAGTTTTGTAATGTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 TGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCTAATCTTA
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                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                  Length 1622;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                    Sequence 1622 BP; 478 A; 354 C; 313 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                            Score 186; DB 17;
Pred. No. 4.9e-40;
0; Mismatches 620;
                                                                                                                                                                                                                                                                               Query Match 10.9%;
Best Local Similarity 52.1%;
Matches 726; Conservative
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                      941
                                                                                                                                                              gtatggtgggatcgactcatgagcaacttgtaggaaatgaagggttgtcggtagctgcaa
                                                                                                                                                                                                                                                                                                  CAGCTATTGGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAAGGCGTTCTTGCAGATG
                                                                                                                                                                                                                                                                                                                                       ccgccatcggagatgctatccataagaggttacatgactacgaaggaattctgagaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGATTTTGGATGGGGAAAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAATTTGACA - - - TTACCTCTGTTGATTATGCAGAATTGATTTATGTGATTCAGTCCA
                                                         TATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATT
                                                                                                taagagagaa---ggtggaagaggataaacatgcagcaacttatgtgctttcatcaact
                                                                                                                                     GCCGAGGACTTCTGACGCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCAT
                                                                                                                                                                                                                   GCGTTGCAAAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTG
                                                                                                                                                                                                                                                                                                                                                                            CAAAAACTIGGTTATCGGAATCTA-----ATGGAATCCCTTCAAAAAGATTTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                   attggatatcgccgcccgatcaacatctgcggcaccaaggtcgacgctcatttatgtcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= Aromatic acyl transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT37311 standard; cDNA to mRNA; 1479 BP
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 3..1343
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95JP-0067159.
95JP-0196915.
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29-JUN-1995;
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TCGATAACTTTGATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAAGGTCATCAA 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACTGTTATCCCT 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gagcaatcggtgccgctcacattcttcgacatgacgtggctgcattttcatcccatgctt 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccagaatetecegttaggetetacaactttgteeetaaattgeegeeeattgtegaagaa 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                         Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour
                                                                                                                                plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATCTTAAGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCATCAATGCTTGGGCCTATATTAACAAA - - - TTTGGGAAAGACGCGGACTTGTTGTCC
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                                                                                                                                                                                                                                                                                                                                                     Six
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1479;
                                                                                                                                                                                                                                                                                                                                              tone changes and allowing new colourations to be produced. Sin specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                           DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
Ξ
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Mizutani
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1479 BP; 420 A; 316 C; 331 G; 411 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 172.2; DB 17;
Pred. No. 2.3e-36;
0; Mismatches 668;
Ė
Kusumi
                                                                                                                                                                                                                Claim 4; Page 65-69; 94pp; Japanese.
Υ,
Fukui
                      Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Fujiwara H,
                                                           WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                    P-PSDB; AAW04725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi:
Matches 701; (
Ashikari T,
                      Nakao M,
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1206 tcgattgatggggagaaatatgcaatgacrctttgtaaagccagggatttcgaaggagga 1265
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                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTTATCGGAATCTAATGGAATCCCTTCAAAAGATTTCTCGGGATTACCGGATCGCCT 1214
                                                                                                                                                                                                                                                                                                                   AAGTTCGATTCGTATGCTGTAGATTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACC
690 ttaccgacggaccgcattcgaccaccaatcaaaattaagaaattg
                                                                             aag.....ggttggattcagtccagagttccaagtttagtccatctctcatctttgta
                                                                                                          ATGACGTGTGGATACGTATGGACATGCATGGTCAAATCAAAAGATGACGTCGTATCAGAG
                                                                                                                                                                                         CITCTGACGCCCCCGTGTCCGCCTAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCA
                                                                                                                                                                                                                                                                                               AAAGCAACACATAAAGAGTTAGTTGGGGATAAAGGGCTTCTTGTTGCAGTTGCAGCTATT
                                                                                                                                                                                                                                                                                                                                                          GGAGAAGCCATTGAAAAGAGGTTGCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                         gcggcggagataaaaaaaaggat---caacgacaagagaatattagaaacggtggagaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGTTGATTATGCAGAATTG----ATTTATGTGATTCAGTCCAGGGATTTTGAAAAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1392 GAAGGCTTTTGCTCTTTGTCATAGTCTCTTTAATAGAACCATATTGCTGCAATAAAGTA
                                             AAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATACGTGTAACGACGTTCACA
                                                                                                                                         gcgattgcagcttatatgtgggctggcataacgaaatcattcacagcagatgaag----
                                                                                                                                                                      GAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCGGATTGCCGAGGA
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gene expression; ss.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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                                                                                                                                                                                                                        Example 6; Page 127; 159pp; English.
                                                   (CLIN-) CLINICAL MICRO SENSORS INC.
26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                              monitoring gene expression.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                            1298 TTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAA
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17-MAR-2000; 2000US-0190259.
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gene expression; ss.
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Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                    (CLIN-) CLINICAL MICRO SENSORS INC.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                             (CLIN-) CLINICAL MICRO SENSORS INC.
                                 26-JUL-2000; 2000WO-US20476
                                                                   17-MAR-2000; 2000US-0190259
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                                                                    8; Conservative 434; Mismatches 264;
        Seguence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                             DB 22;
                                                        Pred. No. 8.7e-20
                                           Query Match 6.5%; Score 110;
Best Local Similarity 1.1%; Pred. No. 8.
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     Length 936;
Score 110; DB 22;
Pred. No. 8.7e-20;
34; Mismatches 264;
                                                   Conservative 434;
     6.58;
1.18; P
                            Local Similarity
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TTATGTGATTCAGTCCAGGGATTTTGAAAAAGGTGTGGAGATTGGAGTATCATTGCCTAA 1357
                                                                                                                        GATTCATATGGATGCATTTGCAAAAATCTTTGAAGAAGGCTTTTGCTCTTTGTCATAGTC 1417
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                                                                                                                                                                                                                                                                                                          AACCCTACTTTCGAGGCGGGAACACCACAACGAGGTTCAATCACTAGAAGGTTGTACTTC 1537
                                                                                                                                       The present invention relates to a composition comprising two nucleic
                                TTTTGGATGGGGAAAGCCTGCAAAATTTGACATTACCTCTGTTGATTATGCAGAATTGAT
                                                                                                  Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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L.1%; Pred. No. 8.7e-20;
Ive 434; Mismatches 264; Indels
                                                     ETM; mismatch; genotyping;
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AAF58262 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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group, useful as labels in allowing repeat analyses on

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gene expression;
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acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                          GCACAACGAAAAGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAAT
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                                                      Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other
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llarity 1.1%; Pred. No. 8.7e-20;
Conservative 434; Mismatches 26
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                           1538 ATAAATTCCAGAGGTCGAATATACACCGTTGTCCTCTGAAAAGTTGAACCTCACACCTGG 1597
                                                                                  CATGGTGTTACGATAGGTATTGTATAATGCCATTATATACTTCCATAAAGTATCCTATGC 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           998 TAACTACTTTGGCAACTGTCTTGCGTCATGCGTTGCAAAAGCAACACATAAAGAGTTAGT 1057
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Gaps
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                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                     AAF58254 standard; DNA; 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0145695
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                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                               gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTAAGTTCGATTCGTATGGTGTAGA
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                                                                      Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 106.8; DB 22; ilarity 0.8%; Pred. No. 6.3e-19; Conservative 434; Mismatches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Page 128; 159pp; English
                                                                                                                                                                                                                                                                                                                      (CLIN-) CLINICAL MICRO SENSORS INC
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17-MAR-2000; 2000US-0190259.
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24-APR-2001 (first entry)
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                                   Oligonucleotide D2004
                                                                                        gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACAACGAAAAAGGCGTTCTTGCAGATGCAAAAACTTGGTTATCGGAATCTAATGGAAT 1177
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                                                                  The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                   266;
                                                                                                                                                                                              Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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llarity 0.8%; Pred. No. 6.3e-19;
Conservative 434; Mismatches 26
                                 Example 6; Page 127; 159pp; English
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Search completed: November 5, 2001, 18:11:15 Job time: 15410 sec Appl Appli Appli Appli Appl

Sequence 1

Sequence Sequence Sequence

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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECONBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Laröner
STREET: 1800 Diagonal Foad, Suite 500
CITY: Alexandria
                       PCT-US95-16930-1
US-08-721-488-9
US-09-004-71-66
US-09-182-816-22
US-09-182-816-24
US-09-182-816-24
US-09-1816-24
US-09-471-528-24
US-09-471-528-24
US-08-471-528-24
US-08-471-340-1
US-08-520-6788-29
US-08-520-6788-29
US-08-98-906-769-144
US-08-906-769-144
US-08-906-769-144
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AGG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEFONMUNICATION INFORMATION:
TELEFAX: (703)83-4109
TELEFAX: (703)63-4109
TELEFAX: (703)63-4109
TELEFAX: (703)63-4109
TELEFAX: REGISTRATION NOW SECULOR SE
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; Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : LENGTH: 7218 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: CLONE: PTSgpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                              November 5, 2001, 18:04:15; Search time 168.74 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                     Gaps
Query Match 4.2%; Score 67; DB 1; Length 7218; Best Local Similarity 2.0%; Pred. No. 2.7e-08; Matches 7; Conservative 221; Mismatches 121; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FRSISED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,137
FILING DATE: Filed Herewith
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APPLICANT: Corley, Neil C.
APPLICANT: Ve. Henry
TITLE OF INVENTION: CAF1-RELATED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
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US-09-027-137-2/c
; Sequence 2, Application US/09027137
; Patent No. 6013450
; GENERAL INFORMATION:
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STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2852 base pairs
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MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COUNTRY: US
ZIP: 94304
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                                                                                                                        1513 TTGTTTTCTATGTTTTTTTTTTTTTTTGTAGGTTATGAAGAAACCGAGTATAAAGGAATA 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1535 CTTGTACGTTATGAAGAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAAAAAAA 1594
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Length 2852;
Score 45; DB 3; Length 285
Pred. No. 0.014;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5198347
APPLICANT: Miller, LOUIS H.; ADAMS, JOHN H.; KASLOW,
JEVIC C.; FANG, XIANGEDOUG
TITLE OF INVENTION: DNA ENCODING PLASMODIUM VIVAX AND
PLASMODIUM KNOWLES! DUFF RECEPTOR
UNDRER OF SEQUENCES: 27
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44.8; DB 4;
Pred. No. 0.011;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER PILING DATE: 1996-03-22
NUMBER: OF SEQ ID NOS: 89
SCOTWARE: Patentin Ver. 2.1
SEQ ID NO 64
                                                                                                                                                                                                                                                  1573 ATGTTTTCAGTTATTAAAAAAAAAAAA 1601
                                                                                                                                                                                                                                                                                         2479 ITTAITITACAAATTAAAACATAAATA 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/554,837
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 64, Application US/08821994A Patent No. 6228643 GENERAL INFORMATION:
2.8%;
56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.81
Best Local Similarity 59.4'
Matches 76; Conservative
Query Match 2.8
Best Local Similarity 56.4
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1595 AAAAAAA 1602
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US-08-821-994-64/c
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LENGTH: 1582 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.77
Best Local Similarity 58.55
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: CDNA
US-08-545-1968-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1442 TAGAAAAAA 1433
                   1595 AAAAAAAA 1604
                                                      1442 TAGAAAAAA 1433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                            RESULT 6
US-08-545-196B-12/c
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                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                   Gaps
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Sequence 10, Application US/08545196B

Patent No. 6080577:
GENERAL INFORMATION:
APPLICANT: MUNNICH, ARNOLD

TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: SURVIVAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                        Query Match 2.7%; Score 43.8; DB 6; Length 3157; Best Local Similarity 64.1%; Pred. No. 0.031; Matches 66; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
2.7%; Score 43.6; DB 3; Length 1582;
Best Local Similarity 58.5%; Pred. No. 0.025;
Matches 76; Conservative 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/545,196B FILING DATE: 19-CT-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNET/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
FILING DATE: 20-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: CDNA US-08-545-196B-10
                     , LENGTH: 3157
5198347-3
             SEQ ID NO:3
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                                       GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MINNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.6; DB 3; Length 1582;
Pred. No. 0.025;
0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENTING SISTEM: C-LUSARD LOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FRARCI, C. J.
REGISTRATION NUMBER: 31,350
REGISTRATION NUMBER: 31,350
RECISTRATION NUMBER: 2121-110P
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     LLP
                                                                                                                                                                                            SSEE: BIRCH, STEWART, KOLASCH AND BIRCH, P. PO BOX 747
FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 12, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09370253; Patent No. 6165792; GENERAL INFORMATION:
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31,196

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REGISTRATION NUMBER:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Emmelo, John
APPLICANT: Van Emmelo, John
APPLICANT: Van Montagu, Maria Helena
APPLICANT: Van Montagu, Maria Helena
APPLICANT: Van Montagu, Maria Helena
APPLICANT: Van Montagu, Marc
TITLE OF INVENTION: EMBRYOS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: VITGINIA
COUNTRY: United States
ZIP: 22331-1404
                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1882;
                                                                                                                                                                                                                                                                                                                                                            2.7%; Score 43.6; DB 4; Length 1 larity 57.2%; Pred. No. 0.027; Conservative 0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
         TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BB-1200
CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/361,467B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1999
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 01-AUG-1989
ATFORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Thorpe, Catherine J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1759 TGCGGAATAATCTATGCA 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1564 AAAGGAATAATGTTTCA 1581
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                                                                                                                                                                                                                                              TYPE: DNA
CRGANISM: Hordeum vulgare
US-09-370-253-1
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-361-467B-4/C
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1533 ITCTTGTACGTTATGAAGAAAACCGAGTATAAAGGAATAATGTTTCAGTTATTAAAAA 1592
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VENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
VENTION: EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 7-JUNE-1995
CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 43.4; DB 1; Best Local Similarity 57.9%; Pred. No. 0.023; Matches 77; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
  010830-027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,467
FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Emmelo, John
De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4, Application US/08484332C; Patent No. 5767374
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: De Greef, Willy
                                                                                                                        LENGTH: 1046 base pairs
                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1593 AAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                            IMMEDIATE SOURCE:
CLONE: 3C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     US-08-361-467B-4
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1470 ATGCATGTATTTTTTTTTTTTTGAGGGGTTCTTTCCTTTATTGTTTTCTATGTTTTTT 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: PERL, ANDRAS
TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1332;
                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 43.2; DB 2; Length 1:
57.4%; Pred. No. 0.029;
tive 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COMUREY: USA
COMPURE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAP Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATE: US/08/326,119A
FILING DATE: 19-OCT-1934
FILING DATE: 19-OCT-1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: LIVNAT, SHAUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 280932000100
TELECHOMINISTATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEFAX: (202) 822-0168
TELEFAX: 02010 NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08326119A Patent No. 6018021
                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS.
LENGTH: 1332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1590 AAAAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1210 GCAAATTTTACATAA 1195
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 57.48
Watches 78; Conservative
                                                                                                                                                                                                                                                                    CDS
57..1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
   90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-08-326-119A-1/C
                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-09-057-762-1
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; LOCATION:
US-08-326-119A-1
   TELEX:
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1473 CATGTATGTTTATTTTTTTGGAGGGTTCTTTCCTTTTATTGTTTTCTATGTTTTTTCT 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1533 TTCTTGTACGTTATGAAGAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAAAAA 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                982 TITITITITITITITITICAAGAAAACTTATAAATCCATTTACTTGTTGGGTTTTGATA 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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US-09-057-762-1/c

S.Sequence 1, Application US/09057762

SEQUENCE 1, APPLICATION:
APPLICANT: PERL, ANDRAS

TITLE OF INVENTION: HANN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: WATCH A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: WATCH A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: WATCH A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 43.4; DB 1; Length 1046; Best Local Similarity 57.9%; Pred. No. 0.023; Matches 77; Conservative 0; Mismatches 56; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/057,762 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: FIPPY GOODELING
OPERATING SYSTEM:
                        FILING DATE: 04-AUG-1989
ATORNEY/AGENT INFORMATION:
NAME: SCHULMAN, RODERT M.
REGISTRATION NUMBER: 31,196
REFERENCE/DOCKET NUMBER: 010830-093
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 836-6620
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-5021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1046 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LIVNAT, SHWUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 280932000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 872-0168
EP 89 402 224.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,119
FILING DATE: 19-CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
INMEDIATE SOURCE:
CLONE: 3C9
US-08-484-332C-4
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2227 AAGAGGTACCAGAAGAAGTGGAAGAGGTACCAGAAGAAGTGGAAGAGGTACCAGAAGAAG 2286
                                                                                                                                        TGGAATACGACGATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAGAGATAG 406
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08719822B
Patent No. 5874527
GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/719,822B
FILING DATE: 09/30/96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GAGOTIS, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US2
TELEPHONE: (212)527-7700
TELEPHONE: (212)53-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Darby and Darby STREET: 805 Third Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium vivax
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illarity 51.3%;
Conservative (
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
                                                                                                                                                                                                                                                     2347 CAGCGGTAG 2355
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Matches 97; Conserv
                                                                                                                                                                                                                    407 AAGTTGCAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-719-822B-1
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                                                         287
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                                                                                                               1470 AFGCATGTATGTTTATTTTTTGGAGGGGTTCTTTCCTTTTATTGTTTTCTATGTTTTT 1529
                                                                                                                                        1530 TCTTTCTTGTACGTTATGAAGAAACCGAGTATAAAGGAATAATGTTTTCAGTTATTAA 1589
                                                                                                                                                                                                                    1270 TITITITITITITITITITITITAGAAAAGCACAGGAAAAGTGACTGCTTAATGTATIAG 1211
                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
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0
                                       Length 1332;
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Pred. No. 0.11;
0; Mismatches 92; Indels 0
                                2.7%; Score 43.2; DB 3; Length 157.4%; Pred. No. 0.029;
tive 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,610
FILING DATE: 19930602
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: GOGOCIS, Adda REGISTRATION NUMBER: 29,714
REGISTRATION NUMBER: 5986/07686
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1873-6237
TELEFRAX: (212)753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08072610 Patent No. 5532133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212,
TELEFAX: (212,
TELEFAX: 23687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
"ver: NUCLEIC ACID
"ver: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium vivax
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                                                                                                                                                                                                                                                                     1590 AAAAAAAAAAAAA 1605
                                                                                                                                                                                                                                                                                                              1210 GCAAAATTTTACATAA 1195
                                   Query Match 2.7%
Best Local Similarity 57.4%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.6
Best Local Similarity 51.3
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: PVMB3.3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CLONE: F
US-08-072-610-1
                                                                                                                                                                                                                                                                                                                                                                                           US-08-072-610-1
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STATE:
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                                                                                                 287 TGGTGGATTTCTATCAACTAGCTGGGAAACTTGGAAAAGATGAAGAAGGGGTTTTCAGGG 346
                                                                         227 AAGGTGCTGAAAACTTTGACGAGACGTGGAAAAAATTAAAGATGGACTGGCCTTAGTAT 286
   Length 3337;
   DB 2;
Score 41.8; DB Pred. No. 0.11; 0; Mismatches
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227 AAGGIGCIGAAAACTITGACGAGACGTGGAAAAAATTAAAGATGGACTGGCCTTAGTAT 286

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PREVENTION OF

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2287 TGGAAGAAGTGGAAGAAGTAGAAGAAGTAGAGGTACCAGCGGTAGTAGAAGTAGAAGTAC 2346
                                                                     347 TGGAATACGACGATGACARGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAG 406
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,309B
FILING DATE: 14-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21,1392
REFERENCE/POCKET NUMBER: 210121.422
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 5, 2001, 18:04:28 Job time: 15068 sec
                                                                                                                                                                                                                                                                          RESULT 15
US-08-557-309B-22/c
; Sequence 22, Application UE/08557309B
; Patent No. 5916572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.65
Best Local Similarity 64.65
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                       2347 CAGCGGTAG 2355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                             407 AAGTTGCAG 415
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-557-309B-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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2287 TGGAAGAAGTGGAAGAAGTAGAAGAAGTAGAGGTACCAGCGGTAGAAGTAGAAGTACAAGTAC 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2167 AAGAAGTAGAAGAGGTACCCGCAGAAGTAGAAGAGGGAAGAGGTACCAGAAGAAGTGG 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 AAGGTGCTGAAAACTTTGACGAGACGGTGGAAAAATTAAAGATGGACTGGCCTTAGTAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 TGGTGGATTTCTATCAACTAGCTGGGAAACTTGGAAAAGATGAAGAAGGGGTTTTCAGGG 346
                                                                347 TGGAATACGACGATGACATGGATGGTGTAGAGGTGACAGTGGCTGTTGCAGAAGAGATAG 406
                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09092458

Petent No. 621861
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES:
ADDRESSE: ADDRESS:
ADDRESSE: Darby and Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 41.8; DB 4; Length 3337;
51.3%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: GOGOTIS, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/17686US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/719,821
FILING DATE: 09/30/96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 12-7
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%;
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Matches 97; Conservative
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COMPUTER READABLE FORM:
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                                                                     1510 TTATTGTTTTCTATGTTTTTTTTTTTTTTTTTTTATGAAGAGAAACCGAGTATAAAGGA 1569
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Length 581;
Score 41.6; DB 2; Length 51
Pred. No. 0.052;
0; Mismatches 34; Indels
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Thu Dec 6 12:43:04 2001

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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em_estpl4:* em_estpl5:*

em_estpl3

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gb_est111:*
gb_htc:*
em_gss_fun:*
em_gss_hum1:*
em_gss_hum2:*

em_gss_hum5: em_gss_hum6: em_gss_hum7: em_gss_hum8:

em_gss_hum3: em_gss_hum4:

em_gss_lnv1:*
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em_gss_other:*
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	estB0:* estB1:* estB3:* estB3:* estB3:* estB4:* estB6:* estB6:* estB6:* estB6:* estB7:* estB10:* est100:*	ss 173: ss 174: ss 174
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

υ

TITLE Generation of ESTS from potato leaves and petioles JOBRNAL Unpublished (2000) COMMENT Contact: Cathy Rouning	The Institute for Genomic Research For clone request: please contact Research Genetics, Libraries		source 1632 /organism="Solanum tuberosum"	/cultivar="Kennebec" /db xref="taxon.4113"	/Clone 15he board and ontiolog	/tissue_type="leaflets and perioles"	/dev_stage="'b weeks old plants" /lab_host="SOLR"	/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol: Tissue was supplied by Dr. Pry (Cornell University)	Leaflets and petioles were isolated from 8 week old	greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in	OUNT 18	ORIGIN	Score 428. DB	Similarity 81.2%; Pred. No. 3.6e-95;	Matches 49/; Conservative U; Mismatches 113; Indels U; Gaps	CTCAGGAGAGGCCATTCTCCAATTCCAATCACTCTCCGCACACGTGTGGCTAGCCGT	Db 631 CICAAAIACGCCGTCGTICTTTCCAGICCCTCTCCGCACGTGTGGCTAGCTGT 572	Qy 903 CACACGTGCGCGCAACTCAAGCCCGAGGACTACACTGTGTACACTGTTTGCTGATTG 962	Db 571 CACACGTGCGAGGCAACTCAAACCGGAGGAATACAACGGTTTACACCGTCTTCGCTGATTG 512	Qy 963 CAGGAAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAAT 1022	Db 511 CCGGAAAAGAGTCGATCCTCCAATGCCGGAGGTTACTTCGGAAACCTAATTCAGGCGAT 452	OY 1023 TITCACAGTGACCGCGGCAGGITTGTTACTAGCAAGCCCGATCGAGTTGGTGGGAT 1082	Db 451 TTTCACTGTAACGGCGGGATTGCTGTTATCGAATCCGATTGAGTTTGCGGCAGGGAT 392	OY 1083 GATACAACCATCGTGAACCATGACGCTAAGGCCATTGATGAAGAAACAAGGGGTG 1142	Db 391 GATTCACCAAGCAATTGTGAATCACGATGCGAAGGCGATTGATGAAAGGAACAGGAGTG 332	Qy 1143 GGAGAGCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTGTG	日の日のようようなどうべきない かいかい 日本	DD 271 AAGTTCGCCGAGGTTTAAGGTGTATGATTTTGGATGTGGGGAAAACCGGGGATATACT 212	QY 1263 GAGGAGTGGTTCGAACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGGAAAAATGG 1322 	Oy 1323 AGGAAGAAGCATTGATGTGGGAGTTTGGAAGCAAATGCTATGGAGAGGTTGGAGA 1382	DD 151 AGGAAGGAATTGATGTGGAGATTAGCTTGGAAATGCTATGGAGAGAGGTTGGAGA 92	QY 1383 AGATAAGAGTTCCTCATGGAAACTGCTTAATTTGCTTAGCTTGGACTCAACTGGCTACA 1442	Qy 1443 CITTATTTATGA 1454	
SUMMARIES	Length DB ID Description	141 BE919635 BE919635	119 AW649974 AW649974 174 BG126859	143 BF051093 BF051093 141 BE919634 BE919634	122 AW928744 AW928744	118 AW618433 AW618433	142 BE920362 110 AW039511 AW039511	119 AW649611 AW649611 143 BF053244 BF053244	146 BF275133 BF275133	118 AW617090 AW617090	173 BG096122	142 BE924264 166 BE353229 BE353229	153 BG446054 BG446054 77 AW731285	143 BF054047	76 AW668525 Aw668525	118 AW617259 AW617259 153 BG441719 BG441719	76 AW728139 Aw728139 103 AI899779 AI89977	120 AW735992	24 AI730615 AM517396 AW517395 AW517396	143 BF053972 24 AI727325	118 AW616992 AW616992	119 AW690825 AW690825 115 AW399665	103 A1901068 A1901068 24 A1730449 A1730449	660 146 BF268244 EB000 641 24 AI730451 AI730451 BNLGH721	146 BF278351 BF278351 122 AW934606 AW934606	24 AI730368 AI730368	ALIGNMENTS		632 bp mRNA EST 02-OCT-2000 potato leaves and petioles Solanum tuberosum cDNA clone sequence, mRNA sequence.	GI:10445711		Solanum tuberosum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	., Liang, F., Ch	., Buell,C
ato C	Core Match Le	71	N (1)	~ ~	(4)	9 (7) (4 (4	0 N	C) C	9 (7)	7 (7) (N (N		-	4 ~ 4	-							-	279.8 17.4 274.6 17.1					BE919635 1 EST423404 por CSTB2C8 3' SC			Eukaryota; V Spermatophyti Asteridae; e	l (bases l	Utterback, T., Ha , C.M., Fry, W.E.,

RESULT 1 BE919635/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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BG126859 649 bp mRNA EST 31-JAN-2001
EST472505 tomato shoot/meristem Lycopersicon esculentum cDNA clone
CTOF13L13 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum
Eukaryota, Vilidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon.

1 (bases 1 to 649)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:408"
/clone="cycofi31.3"
/clone="type="shoot/meristem"
/tissue_type="acveloping shoots from 4-6wks old plants"
/lab_host="SolR"
                                                                                                            630 CACCTCAATTTCTGTCCCACCATTCCTTGAACGAACCAAGGCTCGTAACACTCGAGTCAA 689
393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTG---ATGAAGAAGGCACCACCACAATTGCA
                         510 TGTGCAGCTCACCAAGCTCAAGGACGGCCTCACCATGGGATTAGCATTTAACCATGCTGT
                                                                                                                                                                                                       570 GCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTC
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Email: http://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   690 GCTCAACCTCTCAACCATCAGATGCACCCGAACATGCTA 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG126859.1 GI:12627047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: CUGI
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KEYWORDS
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Jaclas, J. Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Giovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="tomato germinating seedlings, TAMU"
/tissue_type="whole seedlings"
/dev_stage="7 days post imbibtion"
/note="Vector: pBlueScript SK('); Site_l: EcoRl; Site_2:
Xhol; 7 days post imbibition on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."

120 c 147 g 178 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 TCTCATCTATAA---AGGTGCTGAAAACTTTGACGAGACGGTGGAAAAAATTAAAGATGG
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                                                                                                            TAMU Lycopersicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.2%; Score 420.2; DB 119; Length 657; 80.7%; Pred. No. 3.1e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.1e-93;
0; Mismatches 118; Indels
                                                                                                        EST328428 tomato germinating seedlings, TAMU Lyco esculentum cDNA clone cLEI11G6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation of ESTs from germinating tomato seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4081"
/clone="cLE111G6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                              Lycopersicon esculentum
                                                                                                                                                                        AW649974.1 GI:7411212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: David Frisch
                                                                                     657 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prime sequence.
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ä 385 GTGGCTGTTGCAGAAGAGATAGAAGTTGCAGATCTTACTG----ATGAAGAAGGCACCACC 441 18; Gaps Query Match 25.3%; Score 406.4; DB 174; Length 649; Best Local Similarity 79.3%; Pred. No. 7.8e-90; Matches 514; Conservative 0; Mismatches 116; Indels 18; = - = = - =

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Local Similarity
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Best Local S
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1 (bases 1 to 642)

Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Liang,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
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kukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida i; Solanalae; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generation of ESTs from tomato fruit tissue, immature green
                                                          CGAGTCAAGCTCAACCTCTCTCAACCATCAGATGCACCCGAACATGCTAAGTCAGCAACC
                                                                                                                                                                                                  ----GACGCCATTCTCCACATTCCAATCACTCTCCGCACGTGTGGCTAGCCGTCACA
                                                                                                                                                                                                                                                                                                                              CGTGCGCGCCCAACTCAAGCCCGAGGACTACACTGTGTACACTGTGTTTGCTGATTGCAGG
                                                                                                     CATGCTGTGCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGAGCTTTGC
                                                                                                                                             AACGGTGATGTCCCGGCCAACGTAGACCCACCTCTTCGCGAAAGAGTATTCAAGTTCTCC
                                                                                                                                                                                                                                                                          GAGTTAGCAATTGACAAAATCAAGTCAACAGTCAATGCCAACTCAGGAGA-----
GTGGATGAGGCTCAAGAATTCAAGTTGCTAATCTTACTGATCATCATGAAGGGATCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tomato,
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/db_xref="taxon:4081"
/db_xref="taxon:4081"
/clone="clEM21F13"
/clone="lb="conato developing/immature green fruit"
/tissue_lb="tonato" developing/immature green fruit"
/tissue_type="fruit"
/dev_stage="lmmature green (5-35 days post-anthesis)"
/dev_stage="lmmature 
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BE919634.1 GI:10445710
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/organism="Lycopersicon esculentum"/cultivar="TA496"
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Pred. No. 2.7e-89;
0; Mismatches 123; I
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al Similarity 78.5%;
503; Conservative
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299 ATCAACTAGCTGGGAAACTTGGAAAAGATGAAGAAGGGGTTTTCAGGGTGGAATACGACG 358
   482 TCATGACTTCCTGGGCCCAGCTTTGTAGTGGGGCCACCTCCATTTCGGTCCCACCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 588)

5 van der Hoeven, R.S., Bezzeridae, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

6 Generation of ESTs from potato leaves and petioles

Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-111-6195, email cdna@fesgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in limit attorem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACCTTACTTAGCTTTTTATTATAACCAAAAGTTGATGGTTTACAAATTAGGGACTGAAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTITGACGAGACGGTGGAAAAATTAAAGATGGACTGGCCTTAGTATTGGTGGATTTCT
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 588;
                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 403; DB 141;
Pred. No. 5.3e-89;
0; Mismatches 95;
                                                                                                                                                                                                                                                                                                        /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db xref="taxon:4113"
/clone="cSTB2C8"
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Solanum tuberosum
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                                   ORGANISM
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AUTHORS
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JOURNAL
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To (bases 1 to 614)

van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /close_lib="tcmatc flower buds 8 mm to pre-anthesis, /close_lib="tcmatc flower buds 8 mm to pre-anthesis, /tissue_type="flower" flower flower buds 8 mm. to-preanthesis" /dev_stage="buds 8 mm. to-preanthesis" /fnote="vector: pBlueScript SK(-); Site_l: EcoRl; Site_2: Xhol; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                           EST337532 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone cTCC2P16 5', mRNA
541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TTCCTTACCTAGCTTTCTATTACAACCAAAAATTTCTCATCTATAA---AGGTGCTGAAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 GCTTTGAGGAAACAGTAGAAAATTGAAAGATGGTTTGGCTTTAGTGTTGGAAGATTTTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CAAACGTGAAACCACATAAACCACTAGGAAAAAAAGAGTGTCAATTGGTAACATTTGATC 181
                                                                                                                                                                                                                                                                                                              30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 112; Indels
                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                           AW928744 614 bp mRNA
EST337532 tomato flower buds 8 mm to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon pennellii
Rukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                      122 CAAACGTGAAACCACATANACCACTAGGAAAAAAAG-AGTGTCAATTGGTAACATTTGAT 180
                                                                                                                                                           181 CTTCCTTACCTAGCTTTCTATTACAACCAAAAATTTCTCATCTATAA---AGGTGCTGAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAACGAACCAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCTCAACCATCAGAT 714
                                                     Gaps
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                                                                                                        AACTTTGACGAGACGGTGGAAAAAATTAAAGATGGACTGGCCTTAGTATTGGTGGATTTC
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                                                     Indels
                  DB 174;
                               .5e-85;
es 122;
                24.1%; Score 386.8;
79 8%; Pred. No. 5.5e
ive 0; Mismatches
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Unpublished (1999)
Contact: David Frisch
                                                 Matches 519; Conservative
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1 (bases 1 to 651)

S van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T., Hansen, C., Ronning, C. and Tanksley, S.

Generation of ESTs from tomato shoot/meristem tissue

Unpublished (2001)

Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: http://www.genome.clemson.edu/orders/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 31-JAN-2001
EST475054 tomato shoot/meristem Lycopersicon esculentum cDNA clone
cTOF24G12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1: Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_llb="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                241
                                                                                    301
                                                                                                                      475
                                                                                                                                                           361
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Eukaryota, Vildiplantee; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
TTACTG --- ATGAAGAAGGCACCAAATTGCAGGACTTGATTCCTTGTAATAAATCT
                                                                                                                                           TGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGCTGTGCAGCTCACCAAGGACG
                                                                                                                                                                                                              GCCTCACCATGGGATTAGCATTTAACCATGCTGTGCTGGATGGTACTTCGACGTGGCACT
                                                                                                                                                                                                                                                                                    TTATGACCTCGTGGTCCGAGCTTTGCTGTGGGTCCACCTCAATTTCTGTCCCACCATTCC
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/clone="cTOF24G12"
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EST

ORGANISM

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

DEFINITION

BG129408

RESULT

ACCESSION VERSION KEYWORDS BASE COUNT ORIGIN

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potato.
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases I to 569)
Van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of Ests from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Hissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in find afform.
  EST424131 potato leaves and petioles Solanum tuberosum cDNA clone
                                                                                                                                                                                                                                                                                                            Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 TACAAAAGTGAAAGTCCTGAAAAAAAAAACGTGAAACCACATAAACCACTAGGAAAAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 TCTCATCTATAA---AGGTGCTGAAACTTTGACGAGACGGTGGAAAAAAATTAAAGATGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GATGGTTTACAAATTAGGGACTGAAAACTTTGAGGAAACAGTGGAAAAATTGAAAGATGG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTG----ATGAAGAAGGCACCACCAAATTGCA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lip="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 363.6; DB 142;
Pred. No. 2.9e-79;
0; Mismatches 89; Ii
                                                                                                                                                                                                                                                                                                                                                                                                            1. .569
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db.xref="taxon:4113"
/clone="cSTB5F22"
        cSTB5F22 5' sequence, mRNA sequence BE920362
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82.3%;
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                                        ACCESSION
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                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                           /clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 371.4; DB 118; Length 582; 79.9%; Pred. No. 3.4e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.4e-81;
0; Mismatches 111; Indels
                                                                                                                                                                     /organism="Lycopersicon pennelli1"
/db_xref="taxon:28526"
/clone="cLPT13E7"
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              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Clemson University Genomics Institute
                                                                                                                                    Location/Qualifiers
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                                                                                            Email: dfrisch@CLEMSON.EDU
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1 (bases 1 to 544)
JACQBL9J., Verballov.J., White,R., van der Hoeven,R.S, Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Giovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum
Sukaryota: Vilidiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/clone="clEisling"
/clone="tope="whole seedlings, TAMU"
/clssue_trype="whole seedlings"
/dev_stage="7 days post imbiblion"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; 7 days post imbiblion on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
a 156 c 131 g 120 t
449
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                                                                                                                                                                                                                                                                                                                                                                                                                                    450 GGACTTGATTCCTTGTAATAAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC
                                                                                                                                                                                                                                                                                                                               510 TGTGCAGCTCACCAAGCTCAAGGACGGCTCACCATGGGATTAGCATTTAACCATGCTGT
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                                                                                                                                                                  393 TGCAGAAGAGATAGAAGTTGCAGATCTTACTGATGAA---GAAGGCACCACAAATTGCA
                                                                                                                                                                                                                                                                                                                                                      AW649611 544 bp mRNA EST304-APR-2
EST328065 tomato germinating seedlings, TAMU Lycopersicon
esculentum cDNA clone cLEI8J16 5', mRNA sequence.
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Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson,
Tel: 864 656 4366
Fax: 864 656 4293
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Contact: David Frisch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 561)
D'Ascenzo, He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,
Bonning, C.L., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,
Fraser, C.M., Verter, J.C., Martin, G.B., Tanksley, S.D. and Glovannoni
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                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
Sukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                       AW039511 561 bp mRNA EST 18-OCT-1999
EST281792 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 TACAAAAGTGAAAGTCCTGAAAAAAACAAACGTGAAACCACATAAACCACTAGGAAAAAA 155
                     511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 prime sequence.
Location/Qualifiers
1.561
/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="cLET14C2"
/clone=Lib="tomato mixed elicitor, BTI
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XII-Blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation of ESTs from tomato leaf tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                clone cLET14C2, mRNA sequence
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AW039511.1 GI:5898265
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/organism="Solanum tuberosum"
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( (pases 1 to 556)

van der Hoeven, R.S., Bezzerides, J., Holr, I.E., Liang, F., Cho, J., Utterback, T., Hanssen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Genration of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF053244 556 bp mRNA EST 16-OCT-2000 EST438474 potato leaves and petioles Solanum tuberosum cDNA clone cSTB34L5 5' sequence, mRNA sequence.
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                                                              Gaps
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Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                           1 | GGGCTTCATAGGCCTCTACTCGCCGTACACCTCACCAAGCTTAAAAGACGGGCTGGCAATG
                                                                                                                                                                                                                                              AAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCAACCATCAGATGCACCCGAACAT
                                                                                                                                                                                                                                                                                                                                                     GTATTCAAGTTCTCCGAGTTAGCAATTGACAAATCAAGTCAAGAGTCAATGCCAACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                      GGAGA-------GACGCCATTCTCCACATTCCACTCTCCGCACGTG
                                    DB 119; Length 544;
                                                              15;
                                                           Indels
                                   Score 355.2; DB 119;
Pred. No. 3.4e-77;
0; Mismatches 93;
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                                    22.1%;
80.1%;
                                   Query Match 22.1
Best Local Similarity 80.1
Matches 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF275133 786 bp mRNA EST 07-MAR-2001
GA_Eb0023D13f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Eb0023D13f, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 TACAAAAGTGAAAGTCCTGAAAAAACAAAACGTGAAACCACATAAACCACTAGGAAAAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 AGAGTGTCAATTGGTAACATTTGATCTTCCTTACCTAGCTTTCTATTACAACCAAAAATT 215
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     petioles"
/cultivar="Kennebec"
/do_xref="taxon:4113"
/clone="CSTB34L5"
/clone="Lib="potato leaves and petioles'
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGATGGTACTTCGACGTGGCACTTTATGACCTCGTGGTCCGA 614
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 353.8; DB 143,
Pred. No. 7.6e-77;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                 158
                                                                                                                                                                                                                                                                                                             130 g
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EST.
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82.3%;
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Matches 428;
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Best Local S
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ORIGIN
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Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

an integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Tel: 864 656 7288
Fex: 864 656 4293
                                                                                                                                                                                                                                                                            /db_xref="taxon:29729"
/clone="GA_Eb0023D13f"
/clone_llb="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATTGCAGGAAAAGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTAATTCA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAATTTTCACAGTGACCGCGGCAGGTTTGTTACTAGCAAGCCCGATCGAGTTCGCTGG 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1077 TGGGATGATACAACAAGCGATCGTGAAGCATGACGCTAAGGCCCATTGATGAAGAAACAA 1136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAGGCTCGTAACACTCGAGTCAAGCTCAACCTCTCAACCATCAGATGCACCCGAACA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
206 c 202 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CAAAGTCCGAAACACCCGCGTGAAGCTGGATCTCTCGCTCCCACCTAACTCTGTCAACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTAAGTCAGCAACCAACGGTGATGTCCCGGCCAACGTAGACCCACCTTTGGCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 786 AGTATTCAAGTTCTCCGAGTTAGCAATTGACAAATCAAGTCAACAGTCAATGCCAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGA------GAGACGCCATTCTCCACATTCCAATCACTCTCCGCACACGTGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        21.5%; Score 345; DB 146;
Llarity 67.6%; Pred. No. 1.2e-74;
Conservative 0; Mismatches 225;
                                                                                                                                                                                                                                  /organism-"Gossypium arboreum"
                                                                                                                                                            Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 719.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                       coli"
                                                                                                                                                                                                                                                                /cultivar="8400"
                                                                                                                                                                                                                                                                                                                                                      /lab_host-"E.
                                                                                                                                                                                                                                                   /strain="AKA"
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Best Local 3
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLET - Inoculated with a variety of disease response
elicitors. Plants exposed to 2.6 dichloroisonicotinic
acid, BTH, jasmonic acid, ethylene, fenthion, EIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was Jestroyed during cloning."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 563)
D'Ascenzo, M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Bonning,C.M., Craven,M.B., Fujil,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Ventér,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum
Sukaryota, Viridizlantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AW041172 563 bp mRNA EST 18-OCT-1999
SET264036 tomato mixed elicitor, BTI Lycopersicon esculentum CDNA clone cLET11N19, mRNA sequence.
                                                                                       1256
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                                                                                                                               693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               GGAGTGGGAGAGCCAACCCGAAGATCTTTCAGTACAAAGATGCTGGAGTGAACTGTGTTGC
                       1197 TGTTGGAAGTTCGCCAAGGTTTCAAGGTTTACGACGTGGATTTTGGATGGGGAAAGCCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BTI "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation of ESTs from tomato leaf tissue Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4295
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 343.8; DB 110;
Pred. No. 2.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF"
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/db_xref="taxon:4081"
/clone="clET11N19"
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                                                                                                                                                                                                                                                                                            Location/Qualifiers
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van der Hoeven, R. S., Bezzeredes, J. L., Matern, A. L., Holt, I. E., Liang
ye, Honsen, T., Craven, M. B., Bowman, C. L., Ronning, C. M., Nierman, W.,
Fraser, C. M., Marthin, G. B., Gloveannoni, J.J., and Tanksley, S. D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW617090 545 bp mRNA EST 24-MAR-2000 EST323501 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT21F17 5', mRNA sequence.
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 90
                              GATGGTTACAGTTAGGGGCTGAAAGCTTTGAGGAAACAGTAGAAAAATTGAAAGATGG
                                                                                                                                                                                TACAAATGTGAACATCTTGAAAAAATCAAATGTGAAGCCACAAAAAACCACTAGGGAAAAA
                                                                                                                                                                                                                                                                                             TGCAGAAGAGATAGAAGTTGCAGATCTTACTGATGAA---GAAGGCACCACCAAATTGCA
                                                                                                                                                                                                                                                                                                                                                           GGACTTGATTCCTTGTAATAAATCTTGAATTTGGAAGGGCTTCATCGCCCTCTTCTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCATCTATAA - - - AGGTGCTGAAAACTTTGACGAGACGGTGGAAAAATTAAAGATGG
                                                                                                                                                             ACTGGCCTTAGTATTGGTGGATTTCTATCAACTAGCTGGGAAACTTGGAAAAGATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC 29634,
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Location/Qualifiers
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100 Jordan Hall, Clemson, SC
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW617090.1 GI:7323200
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AW617090
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completed: November le: 14891 sec

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nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGTTGATCCTCCAATGCCAGAAAGTTACTTCGGCAACCTAATTCAGGCAATTTTCACA 1029
                                                                                                                                                                   181 GGCGACATTAGCGCCCAGCGTGGATCCACCTATGCGTGACAGGGTGTTCAAGTTTTCCGAA 240
                                                                                                                                                                                                                                                                                                           ACGTCGTCGTTCTCTACTTTCCAATCCCTCTCCGCGCACGTGTGGCTAGCTGTCACAGG 360
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                                                                                                         Indels
                                                                                    DB 118;
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Pred. No. 1.6e-71;
0; Mismatches 108;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2569.021 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                        1344157 seqs, 7733874588 residues
                                                          November 5, 2001, 16:46:27
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Listing first 45 summaries
                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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gb_htg9:* gb_htg10:* gb_htg11:*

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gb_htg2:* gb_htg3:*

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gb_un: * gb_vil: * gb_vi2: * gb_htg1:*

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gb_htg5:* gb_htg6:* gb_htg7:*

em_vi:* gb_sts1:* gb_sts2:* gb_sts3:*

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gb_htg22;* gb_htg23;* gb_htg24;*

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E12756 AB029340

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AB026494 E12757 AB010708 E12753 AB016892

1622 1508 1679 1703 66237

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Description

SUMMARIES

gb_in4:* gb_pr10:* em_ba3:*

gb_ro1: gb_ro2: ö

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100.0%; Score 1478.6;
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1; Mismatches
                                                 Location/Qualifiers
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/db_xref="taxon:32644"
a 316 c 331 g 411
                                                                                        411
                    /tissue_type='leaves
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Matches 1478; Conservative
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CIINI5/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
                                                                                                                                                                                                                                                                                                             AL356956 Human DNA
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acyltransferase, partial cds.
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PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASSHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified.
unidentified.
unidentified.
unclassified.
1 (bases 1 to 1479)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukul,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
Gene Cobing PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 4 18-MAR-1997;
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        AC003027
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JP 1997070290-A/4.
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JP 1997070290-A/4
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VERSION
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JOURNAL
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CTCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCAT 240
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/organism='Perilla ocimoides'
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/product='acyltransferase'
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Location/Qualifiers 11476 /organism="Perilla frutescens" /db_xreff="taxon:48386"	/tissue, type="leaf" <pre>/tissue, type="leaf" <pre>/t. :1343 /codon_start=3 /codon_start=3 /product="anthocyanin acyltransferase" /protein_id="BAA93475.1" /db_xref="G1:7415646" /translation="virtureverperposvaegsveltFedmTwLHFHPMLQLLEYEFPC /kranslation="virtureverpykLipt PreESDRKLEVOYENQVTLEPGRGWGIGIAT /kranslation="virtureverpykLipt PreESDRKLEVOYENQVTLEPGRGWGIGIAT /kranslation="virtureverpykLipt PreESDRKLEVOYENGWGWGIGIAT HHTVSDAPSFLATTAWSSNSKHTENEDEDEEFKSLPVFDRSVIKYPTKFDSIYWRNA LKFPLQSRHPSLPTDRIRTFVFTOSKIKKLKGWIOSRVPSLVHLSSFVAIAAYWWGG ITKSFTADEDONEDAFFLIPVDLRPRLDPVPERYFGOLLSYALDAYWWGG ITKSFTADEDONEDAFFLIPVDLRPRLDPVPERYFGOLLSYALDRYWMGG ITKSFTADEDONEDAFFLIPVDLRPRLDPPVPERYFGOLLSYALDRYGADFGW GRARKOETISIDGERYANDKRILETVERWASPEIRKALQKSYFSVAGSSKLDLYGADFGW GRARKOETISIDGERYANDKRILETVERWASPEIRKALQKSYFSVAGSSKLDLYGADFGW</pre></pre>	419 a Similari Similari Z; Cons TGATCGAA		CCCCGGAAAAATGCCGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTCACCATCG 300 CCCCGGAGAAAATGCCGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTTC	AAGTTTTCGCCGTGCAGGTGACTTTTCCCAGGCCGAGGCGTCGTATTGGAATAGCAA 480	ATAGATCCGTCATAAAATTCCGACGAAATTTGACTCCATTTATTGGAGAAACGCGCTAA 660 AATTTCCTTTGCAATCTCGTCATTCCCTCATTACCGACGCGCCCATTCGAACCACGTTCG 720
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 TTTTCACCCAATCCAAAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCAAGTT
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mzautani,M. and Kusumi,T..
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 2 18-MAR-1997;
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                                                                                         FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
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Pred. No. 9.5e-43;
); Mismatches 661; Indels
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35. .1474
/product='acyltransferase'
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SWYNLS?FTVTSALIWTCLSKSLDTVVREKVEEDKRAANLCAFINCRQRFAPPIPQNY
FGNCIVPCMVGSTHEQLVGNEGLSVAATAIGDAIHKRLHDYEGILRGDWISPPRSTSA
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                                                                                                                   Unpublished (1999)

2 (bases 1 to 1622)

Tanaka,Y. and Yonekura-Sakakibara,K.
Direct Submission
Submitted (21-4PR-1999) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Tanaka, Suntory Ltd., Institute for Fundamental Fwakayama-dai 1-1-1, Shimamoto, Osaka 618-8503, Japan
(E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807, Fax:81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GTGATCGAAACGTGTAGABTTTGGGCCGCCGCCGGACTCGGTGGCGGAGCAATCGGTGCCG
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Yonekura-Sakakibara, K., Tanaka, Y., Fukuchi-Mizutani, M. Fujiwara, H., Fukui Y., Toshihiko, A., Yamaguchi, M. and Molecular cloning and biochemical characteization of hydroxycinnamoyl-CoA:authocyanin 3-O-glucoside-6-O-hydroxycinnamoyltransferase from Per frutescens and diverse plant acyltransferase homologs
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GTTGACAAATCCAATGGAGATTCATTAAAGTTCCTTCCACTTTCTTCTTCTACCTATGTAC
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                                                                                                                                                                                                                                                        OS Senecio cruentus
PN JP 1997070290-A/5
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CGTGATCGAAACGTGTAGAGTTGGGCCGCCGGCCGGACTCGGTGGCGGAGCAATCGGTGCC
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T..
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
Patent: JP 1997070290-A 5 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.9%; Score 190.6; DB 10; Length 1508; Best Local Similarity 49.6%; Pred. No. 5.7e-36; Matches 676; Conservative 0; Mismatches 654; Indels 33;
E12757 1508 bp DNA PAT 24-JU
Senecio cruentus mRNA for acyltransferase,,partial cds
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Location/Qualifiers
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/clone='pCAT48'
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/db_xref="taxon:32644"
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                                                         E12757.1 GI:3251589 JP 1997070290-A/5.
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Direct Submission
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                                                                                 ORGANISM
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TITLE
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FEATURES
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Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,
complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941 CGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGCGGCGAGAGCTGGTGGGAGAAA 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           899 GTTCATAATCACCATTGATGTCGATCTCGTCTTGATCCACCAATTCCCACACGTT 958
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                                                                                                                                           TATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAAC
                                                                                                                                                                                    ACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA
                                                                                                                                                                                                                               GCCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAATTTAAAATC
                                                                                                                                                                                                                                                    TITGCCAGTITTCGATAGATCCGTCATAAAATATCCGACGAAATTTGACTCCATTTATTG
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                                                            TAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCCAGGCCGAGGCGTCGG
                                                                                                                                                                                                                                                                                                                                                   TCCACCGGTTTTTGATAGAT - - - TGATTAACATCCCACATTTAGATGAAAATAAGTTGAG
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1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1326 CTGGGAATTAATGGTTAATAAATGTAATTAAACTAATATTATTATTATGTAACAATTAA 1385
                                                                                                                   518
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CCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAA
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                                                                                                                   GGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCG
                                                                                                                                            498 GGCATAGCCGTGGCTCTGACGGCACATCCATTGCAGATGCTAAAAGTTTTGTAATG
                                                                                                                                                                                           795 AAGAACAAAGTACTGAATCTCAGAGGATCCGAACCGACAATACGTGTAACGACGTTCACA
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                                                                                                                                                                                                                                                                                                                       ACATITIGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTTTGGAAGCAAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                          FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product='acyltransferase precursor'
                                                                                                                                                                                                                      1 (bases 1 to 1703)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATANT: JP 1997070290-A 1 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 1703;
                                                                                        E12753 1703 bp DNA PAT Centlanatriflora mRNA acyltransferase, complete cds E12753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product='acyltransferase'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /variety='japonica'
/tissue_type='petal'
/clone='pGAT4'
6. 1415
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0; Mismatches 668;
               1386 TTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT 1422
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/organism="unidentified"
/db_xref="taxon:32644"
a 350 c 359 g 48"
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JP 1997070290-A/1
18-MAR-1997
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49.58;
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Matches 701; Conservative
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Submitted (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Departnent of Plant Gene Research; 1532-3, Yana, Institute, Departnent of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 129-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3934)
Address for correspondence: Aaos@kazusa.or.jp
Robert information on annotation of this clone, please see http://www.kazusa.or.jp/Kaos/cgi-bin/agd_graph.cgi?c=MKF12
Genes with similarity to proteins in the databases are described in 'prodein' or 'or 'orde' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory, http://compbio.orml.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), GENSCAN (Chris Burge, MIT, http://ccanford University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and splicePredictor (Volker Brendel, Stenford University, http://gremlinl.zool.lastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/cddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is Kl386 and the 3' clone is K3K3.
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vsgrnwtaehqkilssnlvnasftaqasyqesgvsqipymtarifrseftysfpvtpg
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Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsul Pl
clone:MXF12.
GAAGGCTTTTGCTCTTTGT'CATAGTCTCTTTAATAGAACCATATTTGCTGCAATAAAGTA 1451
                                                                                                                                                                                                                                                                                                                              27-DEC-2000
5, Pl clone:MXF12
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covered by
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Structural analysis of the regions of 1,081,958 bp covere
Seventeen physically assigned Pl and TAC clones
DNA Res. 5 (6), 379-391 (1998)
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/product-"receptor-like protein kinase"
/protein.id="BMB10814.1"
/db_xref="GI:10177545"
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                                                                           TTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT
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/note="gene_id:MXF12.2"
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2613. .5234
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/translation="MGNKKLLTGGSSKTHGSGSSYRDPLLQNQEDKPKANGSENGLND
LEHGVVEAANGFGRVFALICQYSSINVSQAKEDGKLV1TALLICSTTHLLVPRK
GGMIIDIUSRDWYFPEQQTEELIAVRNAVYILLILVGSTCTALRAWLENGSSERVV
ARLRKDLFRHLMHQEIAFYDVTKTGELLSRLSEDTQIIKNAATTNLSEALRNVTTALI
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VRTVRSFAKESYMVSQYSKKVDETLKLGLKQAVLVGLFFGGLNAAFTLSVITVVSYGA
YLTIYGSMTVGALTSFILYSLTVGSSVSSLSSLYTTAMKAAGASRRVFQILDRVSSMS
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GEASFTDIENAAKMANAHEFIEAFPDKYNTVVGERGLRLSGGGRQRIAIARALLTNPS
VLLLDEATSALDAESEYLVQDAMDSLMAGRTVLVIAHRLSTVKTADCVAVISDGEVAE
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34363. .35709
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FGVYGLDFGWGRPEKVVVVSIDQGEAISFAESRDGSGGGVELGFSLKKHEMDVLVDLLH
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complement(join(30804, .30874,30947, .31289))
//note="contains similarity to Ac-like transposase
gene_lanxF12.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27466. .27879,28046. .29073))
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17337. .17461.17541. .17640,17403. .17974,18073. .18131,
18285. .18395,18488. .18532,18712. .18844,18934. .19009,
19232. .19297,19385. .19492,19591. .19698,19873. .20070,
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LTLUNLFRPSNNSLAFVNGIEIVSMPDRFYSKGGFDDLTVKASIPESKSLIKEFIVPVY
UTLANVGGHWUDEVNDSGMERMLSDDYEFLIGGVSPYMPDVNISYTEKTPAYVAPAY
VYSTCKMMGNAQDTYLALNFNLTWLFTVDAGFSYLVRLHFPERXYLKANORVFSIFLG
NQMAREEMDVIRLSGGPRIPITYLDFRIYUGSESGPRPDLRLDLHPLVKDNPEYYEAII
NGREILKLINNSGNLAINDNELKPUPSLSNLTPNHTVQIKGKSSHLLVKIPTKATG
GGGLAFTVVVLMLWARKQMKRKNRKERVVVFKKLLANYTYRELK TITKSFSYIIGKGS
FGTVYGGNLSNGRKVAVKVLKDLKGSAEDFINEVASMSQTSHVNIVSLLGFCFEGSKR
                                                                                                                                                                         YDAILNGVEIIKMNDEDGNLÄGENEDELVSPOLIPNRAFPRIRKNKSHILPITLAVVG
SLYVLAMFVGVLVIMKKKSKPSTNSSWCPLPHGTDSTNTKPAKSLPADLCRRFSI
EERSATNDFEDKLIIGVGGEGSVYKGOIDGGATLVAVKRELTSNGAREFFELEM
LSKLEHVHLVSLIGYCDEDNERVLYYEYMPHGTLKOHLFRRDKTSDPPLSWKRRLEIG
IGAARGLQYLHTGAKYTIIHRDIKTTNILLDENFVTKVSDFGLSRVGPTSASQTHVST
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SYREINNGGOTVNEVDDSGMRRMLSDDSFGNRGSIVNVPGYKINYTERTPAYVAYD
VYATSKLMGNSSNLMFRULGGMFRWLSDDSFGNRGSIVNVPGYKINYTERTPAYVAYD
VYATSKLMGNSSNLMFNLTCHFTVDAGYTVLJRFLEFTPQYTKAGQRVFSIFVD
KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTNQTYYDAIL
                                                                                                                                                                                                                                                                                                                                                                          VVKGTFG*LDPEYYRRQVLTEKSDVYSFGVVLLEVLCCRPIRMGSVPPEGADLIRWVK
SNYRRGTVDD011DSDLSADITSTSLEKFCETAVRCVQDRGMERPMNDVVMALEFALQ
LHTAAKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
SGSSWGVFSEINEPRAR"
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GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MNCNVLETLSVLVSVTACVTAAVHPTDVPLFNCGDTSNNVDNSG
RNWTVESRQILSSNLVNASFTSEASYQKAGVSRIPYMKARIFRSEFTYSFPVTPGSIF
LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
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LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQYIYAELKKITKSFSHTVGKGGFG
TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
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SYGMLVLDMIGARNKVETTTCNGSTAYFPDWIYKDLENGDQTWIIGDEINEEDNKIVK
KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
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WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSFGWKFL
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QNILLDGNLCPRVSDFGLAKLCEKRESVLSLMDTRGTIGYIAPEVFSRMYGRVSHKSD
VYSFGMLVIDMIGARSKEIVETVDSAASSTYPPDMIYKDLEDGEQTWIFGDEITKEEK
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                                                                                                        PDDVYATSRSMGNADHPEQNLNFNLTWLFTVDAGFSYLVRLHFCETLSEVNKEGQRVF
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                                                                                                                                                     SIFIENQTATLEMDVFRMSGSWIPMYLDYTVIAGSGSGRRHDLRLDLHPLVSINPKY
SNFLRLYFYPTRYGSQFNAVKSFFSVKVNGFTLLNNFSADLTVKASKPQTEFIIKEFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="receptor protein kinase-like protein"
/protein_id="BAB10826.1"
/db_xref="GI:10177547"
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unknown protein"
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                                                                                                                                                                                                                                                           TCGAAGAATCCGATAGAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCCAG
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ISPQTFTSSPSLSPSSSSGGSSFWARPYAMESSKQLANGLINLGDMGYKTLSKYCQDML
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INCHSKPGSIESAESSEEGSTKQMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
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EVFFGEEGGVLMVSANSSMDLADLGDLFVPNPAWLPLIFRNPGEEAYXILEMPLLIAO
VTFFTCGGFSLGIRLCHCICDGFGAMQFLGSWAATAKTGKLIADPEPVWDRETFKPRN
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SSVESLINDSLSKTRLVQDARLEYSEDYLSSWYDYDVRRPKELEFGKLJITOWTR
FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPAVHT
Submitted (15-JUL-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (bases 1 to 101176) Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chio, J., Choi, E., Conn, L., Comway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Direct, Submission
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/note="unknown protein; simila-"
/note".unknown protein; simila-"
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/db_xref="taxon:3702"
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complement(4838. .6223)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTCGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGCGAGAGCTGGTGGGAG
                                                      2 CGTGATCGAAACGTGTAGAGTTGGGCCGCCGCCGGACTCGGTGGCGGAGCAATCGGTGCC
                                                                                                                                                                                                                                                                        GCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAA - - - AACT
                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAATTTAAAATCTTTGC----
    DB 12; Length 101176
                             35;
                             Indels
                           0; Mismatches 692;
  Score 110.8; DB 1
Pred. No. 3.3e-16;
 7.58;
Query Match
Best Local Similarity 47.2'
Matches 651; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536
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Federspiel, N.A., Fallm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B. I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

Li Submitted (12-OCT-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto, CA 94304, USA

E J (bases 1 to 119914)

E Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 119914)
1 (bases I to 119914)
Altafi.H., Araujo.R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S.,
Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S.,
Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                38409 CCCATTATCCAACCTCAATHGCAGGAGCTCCGAAATTGGGACTGTATGACATGGATTTTG 38468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38526 CATTCTCAGACTCCAGAGAGGCAGCAATGGAGTTGAGATTGGAATAGCACTAGAGAAGA 38585
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Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
Submitted (30-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTTTGTAAAGCCAGGGA!TTTCGAAGGAGGATTGGAGGTTTGCTTGTTTTGCCTAAGG 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA PLN 30-JAN-1999 chromosome I BAC F21M11 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1294 ACAAAATGGATGCTTTTGC%GCTTATTTTTCACTGGGAATTAATGGTTAATAAATGTA 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGGGGGAAGGCGAGAAAGCAAGAATATTGTCGATTGATGGGGAGAAATATGCAATGA
                                                                                                                      ACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGA
                                                                                                                                                                                                   GCGA----TCTGTTGAAGACAGCACCAAGATGGGGACAAGGAGTACGTAAATGGGTCATGT
                                                                                                                                                                                                                                                                                    AATCATATT - - - TTTCGGTGGCAGGATCGAGCTAGATCTTTACGGTGCAGATTTTG
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Arabidopsis thaliana
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COMMENT

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.21994,
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/Lanslation="MLOGISGHTHEKLSVETAEPHHLNDRYHIVEEIPKASVIPITE
ICDEAEEKCSPSTISRKRYTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
TOOLITEASNSGSYPENHYKNCRESDDDLEEDEPCOSDDLDEDERYSDVGFSE
DSLIHPPTREYTQDIGMTEEIDSKLKSSK
SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDDQIDDITLSVWFKCRIEPKKLRNQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAVDASĽSTWĽSTSESGSECNSASMYTLTPEKLKŠTSCYSKPLRINHDDRPVLCALŤL
EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
REDKSVNWHSTPFEARLEKALNNIDK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MGSSSPEARARAQVPSMILIFLEIICTVHVYTNRRKLNRDVLSA
NLNIPKRVTRRDLRFMESVISIYKSLNAAVSVHLPQLQIPNDCNYKNDALNNSNSPKH
GESEDSEMTDKDVSKRSGGTDSSSRDGSPLPTSEESDPRPKHQDWTEKQLSDHLLLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FESETDAANHTPESTTEGAAKNYRDITASEQPSNAARKRICGESFIGESSPNPKTODP
TLERAMESLESDDPTDVYRAQNHQWYSTEWUTSTSVLLCLRSNBLRCVVTCVQQLPK
SHTEQDSKRKRDITASDAMENHLKVPKRENNLAGKSNDLCVVTCVQQLPK
KALEQTSSNITICGFCQSARVSEATGEMLHYSRGRPVDGDDIFRSNVIHVHSACIEWA
BOYYEGGDTNKNLKABELARGMXIKOTKKCSLKGAAAGGFVKASCRRSYHVPCAREISRCR
WDYSDGPLLLCPAHSSVKFPWRKSGHRVSRABELDFKINPCAELSRCR
WDYSDFLLLCPAHSSVKFPWRKSGHRVSRABELDFKINPGSLEGSLEGOTPAFTKELVLCG
SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILLNGKW
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GDFYKGYKEDLONLVKVAGGTILNTEDELGAESSNNVNDORSSSIVVYNIDPPHGCAL
GEEVTIIWORANDAEALASOTGSRLVGHTWVLESIAGYKLHPVIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIPGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKWCVEFGIEANAIVAVPYDWRLS
PTKLEERDLYFKLKLTFETALKLRGGPSIVFAHSMGNNVFRYFLEWLRLEIAPKHYL
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DTGLEKALIEDYDDDSKRWHOLKKYRYPFRYINIAHRSSLGAFLLXHDDPVENPLTPW
BRPPIKNYFCIYGAHLKTEVGYYFABSGKYPDDWIITDIIVETEGSLVSRSGTVVDG
NAGPITGDETVPYHSLSWCKNWLGPKVNITMAPOILIGKIKQQPEHDGSDVHVELNVD
                                                         complement(join(14567. .14641,14787. .15831,15906. .16006,
16327. .16362)}
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAD10668.1"
/db_xref="G1:4204287"
/translation="MGANSKSVTASFTVIAVFFLICGGRTAVEDETEFHGDYSKLSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(16835. 17185,17274. 17392,17491. 17656, 17795. 17885,17982. 18079,18175. 18361,18504. 18604, 18705. 19049,19134. 19349,19439. 19791,19862. 19967, 20188. 202338), /gene="F21M11.4" //note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLPVSEGTARLLSNSFASSLWLMPF
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22102. 22178,22542. 22758,22920. 23064,23343. 23442,
23599. 23693,24021. 24072,24227. 24298,24441. 24647)
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gb|H76794 and 203124XP, gb|AA605510"
                                                                                                                                                                                        /note="Unknown protein; Location of ESTs 40C3TT, gb|AA728590 and40C3T7, gb|T04573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
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       complement(14004. .16362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(16835. .20238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="AAD10669.1"
/db_xref="GI:4204288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAD10670.1"
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/gene="F21M11.6"
27777. .28734
/gene="F21M11.6"
/gene="F21M11.6"
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/gene="F21M11.5"
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       gene
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/translation="MDRFMFISITIASILVGVVSAGDWNILNOLRGLGSSSSONGIVS
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LHFGSNCCSKSKCDGMDAWIFDIDDTLLSTIPYHKKNGFFGGEKLNSTKFEDWIQKKK
APAVPHMKKLYHDIRREGIKIFLISSRKEYLKSATVDNLIQAGYYGWSNLMLRGLEDO
GKEKQYKSERRKWLMSLGYRWGVWGDQWSSFAGCPLPRRFFKLPNSIYYVA"
complement(join(14004. .14312,14565. .14641,14787. .15831,
15906. .16006,16327. .16362))
On Dec 30, 1998 this sequence version replaced g1:2734094.
Bases 1-9262 of clone F21M11 overlap with bases 6898-78259 of
"TAMU' BAC clone F20022 (AC002411), and bases 119525-119914 of clone
F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAYKULLDAIFDEADAQSTEKNKKEEEKKKREEEKKSRSVATSRGRRKAPEPLVQDEE
DDOEDDEFPERKRLSRRRASSSSSSSSSSRVANDELKRYDFEEDEDGOVTELPPLKRY
VRRMGERGLAMTVANSSPSSSRLSMEDERPPWTLLPAHPWETKSEASALVILN
EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SHKVAAASVELASSTSGEAKICLSFPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
VHPREVSVLGFMKDMSSYSJSGAKICLSFPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
VHPREVSVLGFMKDMSSYIDLARSTSOLLETETVOMSKAGDESGANGISMPLVVVP
ECEISGDGWKAISNMKDITAGEENVEIPWVNEINEKVPSRFRVMPHSPYGDDAVIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAD10665.1"
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KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                                                                                                                                                                                                                                   as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Proteins in this region are annotated in the F21M11 entry, AC002411." 11...9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDQ
                                                                                                                                                                                                                                                                                                                           unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                    e-mail for correspondence: arabésequence.stanford.edu
denes with similarity to proteins in the databases are described a
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="overlap with bases 68998-78259 of 'IGF' BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTMQILNKA"
join(13033. .13488,13717. .13926,14139. .14514)
/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9833,10033. 10256,10344. 10410,10501. 10551,10685. 10781,10885. 10913)
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gene="Filml1.2"

/note="Similar to acid phosphatase; Location of ESTs

110c277, gb|142036, and 110c2xP, gb|A1100245"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/chromosome="1"
/clone="F21M11"
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/gene="F21M11.1"
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/gene="F21M11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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WO0032789.
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/codon_start=1
/protein_id="CAC09066.1"
/db_xref="GI:10187185"
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Sequence 40 from Patent
AX025514
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JOURNAL
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KEYWORDS
SOURCE
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/translation="mntkTmrlPprrylladkrkErdafisSyTdnppElakfpSpPp
KLVPPpvnpiskkSstaaaepigSnQlmLaGylsHEYLTQGTLFGEQWNQaraQaESS
KIRPSHTVEPAEECEPKRKRYREVANLLRSDGAQLPGIVNPAQLARFLKL"
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                                                                                  .31587,
                                                                                                                                                                                                                                                                                                                             45957 TCATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTCCATCAACCACTCTTCCTC 46016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | || || CGACCCTCCATATTACACTACAACGATGGCCAAGACTCTCTTTTTTTCACCGTAGCAG 46256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46796 TTGATCAAGACACTTGTACAAGACAGTGAAACAAAGGCCAACGAGGAAGACAAGGATGAA 46855
                                                                                                                                                                                                                                                                                              46017 TCACCTTCTTCGATGCCCCCTGGCTCTCTCTCCCCACTCGCCGATTCTCTTCTTCTTCT 46076
                                                                                                                                                                                                                                                                                                                                                                                                                               46137 TCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCCCGCCTCGTC 46196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46676 GCCACTTTTACATTGAGCCGGAAGCAGATAGATAATCTAAAAAGTTGGGTTACAGAGCAG 46735
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                                                                                                                                                                                                63
                                                               /gene="F1M11.7"
complement(join(29264. .31015,31312. .31414,31484.
31782. .33033))
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                                                                                                                                                                                                4 TGATCGAAACCTGTAGAGTTGGGCCGCCGCCGGACTCGGTGGCGGAGCAATCGGTGCCGC
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                                                                                                                                Length 119914;
                                                                                                                                                               Indels
                                                                                                                              Ouery Match 6.7%; Score 99.6; DB 12; Best Local Similarity 47.3%; Pred. No. 1.8e-13; Matches 657; Conservative 0; Mismatches 684;
                                                complement(29264. .32033)
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Tunen, A.J.

Fruit flavour related genes and use thereof
Patent: WO 0032789-A 40 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN
JOHANNES VAN (NL)
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ITLFPNQGFSIGVSSHHAILDGKTSTLFLKSWAYLCKQLQLCHHPCLSPELTPLLDRT
VIKDPTGQDMLQLNKWVVGSDNSDPQKIRSLKVLPFLDSESLNKLVRATFELTREDIT
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Sapindales; Rutaceae; Citrus.
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IIVGFTADYRSRLDPPIPLNYFGNCNGRHCETAKASDFVQENGVAFVAEMLSDMVKGI
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NPPVERLFFYEMTDLTWDLFNSEILPKLKHSLSFTLLHYLPLAGHIMWPLDAAKPAVY
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Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and
                                                                       46916 CCACAAACATACTTTGGCAACTGTATGGCTCCTGGTATCGTATCAGTCAAGAACACGAT
                                                                                                                                                                                                                                                                                                                                                 1164 GCAGATTTTGGATGGGGAAGGCGAAAAGCAAGAATATTGTCGATTGATGGGGAAAAA
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Address for correspondence: kaos@kazusa.or.jp
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.egi?c=wDDi
Genes with similarity to proteins in the databases are described
Genes with similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://gronnen.wustl.edu/eddy/tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://gronnen.wustl.edu/eddy/tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is Ti3Jil and the 3' clone is T26G12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //cvidence=not_experimental
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/product="anthocyanin 5-aromatic
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VAAHHAVLDGFTSZFTKAMAQICKQELQSMPENLLTFSTDRSILKYPTYLDERMIELY
RSLKEDQINIRSLTSLPSSKLGDDVVLATLVLSRADIERLREQVKNVSPSLHLSTFVI
Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones
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FWEEKGFVTAAEI I SDLVKGLSSRK I ET I ADTFVEGFSFQSWSTQFGT I AGSTRLGVY
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                                                                                                                                                                                                    2 (bases 1 to 85690)
Kaneko, T., Kato, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
Direct Submission
                                                                                                                                                                                                                                                                                              Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
                                                                                                                                                                                                                                                                                                                          Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains similarity to TNP2-like transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(10671. .10844,10921. .11208)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .85690
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                                                                                                                      DNA Res. 7 (3), 217-221 (2000) 20363099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  emb|CAA16722.1
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                  DADAIEANDDKVSEILEILKEGAMIFSVAGSTQFDVYGSDFGWGRPKKVEIVSIDRTQ
AISLAERRDGGGGVEVGVVLEKQQMEVFESVFADGLKNDLV"
1 344 c 354 g 486 t
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Magnollophyta, eudicotyledons, core eudicots, Rosidae, eurosids II,
Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                   990 AGCTAAATTAGCCAAAGCCAAAACTGAAGCTGAAGCTGCAGCAGGTAATGATGAATTAA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1050 AAATATTATTGTGGGGATTCACTGCGGGATTATAGGAGCCGTTTGGATCCTCCAATTCCACT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1168 GTTCAAGAAAATGGGGTTGCT-TTTGTTGCAGAGGTGTTAAGTGATATGGTCAAAGGGAT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1112 GCAGAA----ATCATATTTTCGGTGGCAGGATCGAGCAAGCTAGATCTTTACGGTGCA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTTTGGATGGGGGAAGGCGAGAAAGCAAGAATATTGTCGATTGATGGGGGAGAAATAT 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTGGAGGTTTGCTTTTG 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1287 CCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAATTAATGGTTAATAA 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1462 GAGAAGCAACAAATGGAGGTTTTTGAATCTGTATTTGCTGATGGACTGAA----AAATG 1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1347 ATGTATGTAATTAAACTAATATTATGTAACAATTAAGTGTTGAGTGTAGGTGAACGTGAA 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATAATCCCTATTATATATTTATGATTTGGTTCAAATAAAGTGTAAAGCCTCTTGAAAA 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1052 CAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTT 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1285 AAAGAAGGAGCAATGATTTTTTTTCTGTGGCTGGCTCGACCCAATTTGATGTTTACGGGTCG 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1227 CGATG--CGGATGCCATTGAAGCCAATGATGATAAGGTTTCAGAAATATTGGAAATTCTG 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                           872 GGATGCATTTTCTTGATTCCGGTCGATCTAAGGCCACGATTAGATCCGCCGGTTCCTGA 931
                                                                                                                                                                                                                                                                                                                       812 AGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATGAAGACCAAGACGA 871
                                                                                                                                                                                                                                                                     Gaps
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Pl clone:MOD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 AAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGCGAGAGCTGGT
                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                       Length 1648
                                                                                                                                                                                              Score 76.8; DB 9; Length 16
Pred. No. 3.4e-08;
0; Mismatches 312; Indels
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                                                                                                                                                                                                                                                            Matches 342; Conservative
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                                                                                                                                                                                                                                   Similarity
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                                                                                 464
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                                                                             BASE COUNT
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AB028618
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VERSION
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SOURCE
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YGTIPQGFVLPTHSRAPVLLSSTRSDLYLSTLSGFVVKYAYVLTKSPSAKEIDDD
IVRVTLQLSQENIKKLKERTKNESTRSDLYLSTFVVKYAYVLTCVVKARGGNVDRPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(48707. .49066,49148. .49372,49477. .49764,49850. .49982,50772. .51282))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15260 AGCCAGTCAAAAGAGTCTTCTTCTACGAGCTCACCGAGTCTACTCGTGACCATTTCCACT 15319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15200 ACTCAGCCAACTTGCACAAACTTCCTTTAACTTTCTTCGACCTTCCATGGCTACTATTCC 15259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15497 GTTATGGACAGCGTCCTTTGTCAGAGTTACATGCCTTGGTTCCCAAGTTACCGGTTTCTG 15556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 TCTCATGCAATTTAATCTACJCTTCATCCCCGGAGAAAATGCCGGGGGTTTCGGTATCTAT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 TCGAAGAATCCGATAGAAAGTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
complement(46109. .47990)
/note="contains similarity to reverse transcriptase
gene_id(MOD1.13"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 ACTCGGTGGCGGAGCAATCGGTGCCGCTCACATTCTTCGACATGACGTGGCTGCATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15380 TCACTGGCCACATCACTTGGGAGCCAAACGAGCCAAAACCGAGCATAATCGTCTCGGAAA
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LLLSTFVVTYEKSSGQSLFCKEEAKKSL"
complement(join(40204. .40603,40656. .40872))
/note="gb|AAC97247.1
                                                                                                                                                                                                /evidence-not_experimental
complement(join(42135. .42706,42772. .43162))
/note-"gene_id:MoD1.11
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                                                                               gene_id:MOD1.10
similar to unknown protein"
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similar to unknown protein"
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/note="gene_id:MOD1.12
unknown protein"
/codon_start=1
                                                                                                                                             /codon_start-1
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VVBSEADFSTISKELRLEFELRPLVPLVPELQVSDSASLLSLQCITLFPRNGFSIGTTVH
HVVMCKTASKFHKSWAHICKHGTPQDFDLPTVLDRTVINVPAGLEGKIFGLSSYIS
EEKDYARTLTLPPAKEIDNDVVRVTLELTEVJIEKLKERAKNESTRSDLHLSFFVVSY
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GKDCYVNGVEILSDSVRGLGSRNIESIWEVYEDGTKNMKLDTQNVTVTGSNQFGIYGS
DFGWGRPVKTDVWSLYKNNEFSMSARRDEIGGLEIGISLKKCEMNVFLSLFTSDFDIY
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ppvplfyfgncvlpidfngyeattflgedgfvngveilsdsvkglgsrslesvwevye
Egtknmkvgtkvlfvtgsngfgiygadfgwgrpvntdvmslyknnsfsmsarrdeigv
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/product="Mutator-like transposase-like protein"
/protein_id="Bab251.1"
/db_xref="GI:11994480"
/translation="MDRLCERDPYYDDMKVAKRAIEQMEMVAMMEGIPKFCPCGGSIV
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EEMOKELKAHRAEIVNVSKVLFRNPMAPKK"
comptement (join (33460 ..33573,33657 ..34016,34094 ..34255,
34330 ..35070,35486 ..35721,35799 ..36093,36146 ..36256))
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ESPMLDDSTFYDALKHIPAEEIQENMQTDEVEDEETETNKELACANPVEEAERQDDGL
TVIEEEEERSSESDEDVNVEKSVEDEGHEDERDEDVIVEKSGEERTIDEDIANVDMEE
AMAMQPLGMYFPVSEYPKKMKLATRCYISEVLKTFADLEHPLTHVEKNYFMEHPSFKH
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WPVBFCVPLEFLAFEAIPSLBERFIEKBEABARGCORACKVNFKRIENGETLADIN
WPLGTTFVIESIIREKAEFVPLLAETTGVEDDYDKHDVVVDSMKRLGGGREIRFEEV
YNEDVQARMEAPNEEEVPTAVGPGDPTLVDVMEKLHSINDKLNEALLVLMEIEEKQAT
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PKLFQLLPYLSKEKVNARNLMLPPAKENINVVRVTLELSEANIKKLKEQAKNESTWSD
                                                                                                                                                                                                /translation="MALNVIKISRVSLVTNSVEPLVLPLTFFDLLWLKLNPIERVTFY
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PASYQSAGNMNFANRYFKTGVIRREDVKTKLMEMEPARSKDRLRMAALYFLTSIIVMP
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complement(36608. .37000)
/note="gene_id:MOD1.9
                                                                               /product-"anthocyanin 5-aromatic
acyltransferase/benzoyltransferase-like protein"
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/db_xref-"GI:11994478"
                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(27960. .28438,28676. .28739))
/note="gene_id:MOD1.5
unknown protein"
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join(32547. .32726,32904. .33122)
/note="gene_id:MOD1.7"
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/db_xref="G1:11994479"
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/protein_id="BAB02522.1"
/db_xref="G1:11994481"
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/protein_id="BAB02523.1"
/db_xref="G1:11994482"
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29217. .31674
/note="gene_id:MOD1.6"
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                                           15902 ATATTGAGAGACTTAGGGAACAAGTCAAGAACGTGTCACCGAGCC---TCCACTTGTCGA 15958
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                                                                                                                                                                  15959 CTTTTGTCATTGCTTACGCTTACGCGTGGACTTGTTTCGTGAAGGCACGTGGAGGTAATA 16018
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                                                                                                                                                                                                                                                                    TC-----ATTACCGACGGACGCATTCGAACCACGTTCGTTTTCACCCAATCCA 735
                                                                                                                                                                                                                                                                                                                                                                                          CTTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATG 855
                                                                                                                                                                                                       632 TGACTCCATTTATTGGA-----GAAACGCGCTAAAATTTCCTTTGCAATCTCGTCACCC
                            GCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTC
                                                                                                                                                                                                                                                                                                                              AAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCCAAGTTTAGTCCATCTCAT
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                                                                                     514 TCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACA--CATTGAAAATGAAGATGAAGA
                                                                                                                                               572 TGAAGAATTTAAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATT
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15557 ATGACTCAGCGA-
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AC069470 136047 bp DNA HTG 19-JAN-2001 Arabidopsis thallana chromosome I clone IGF-F7F7, *** SEQUENCING IN PROGRESS ***, 4 unordered pleces.

DEFINITION

AC069470

ACCESSION

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

Lin, Kabl, S., Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M., Roo, H., Fulji, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L., Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker
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                                                                                                                                                                                                                                                                                        Town, C.D. and Kaul, S.
Town, C.D. and Kaul, S.
Direct Submission
Submitted (01-300-2000) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Jan 19, 2001 this sequence version replaced gi:12280790.
* NOTE: This is a "vorking draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTCGGTGGCGGAGCAATCGGTGCCGCTCACATTCTTCGACATGACGTGGCTGCATTTTC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 TCTCATGCAATTTAATCTACCCTTCATCCCGGGGGAAAATGCCGGGGGTTTCGGTATCTAT
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Pred. No. 1.5e-07;
0; Mismatches 651;
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/Organisma-Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"___
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Eukaryota; thallana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Magnoliophyta; Eusasicaceae; Arabidopsis.

I (bases 1 to 136047)
Lin, X., Kaul, S., Town, C.D., Benito, M., Creasy, T.H., Ronning, C.M.,
Koo, H., Fujii, C.Y., Utterback, T., Barnstead, M.E., Bowman, C.L.,
White, O., Macman, W.C. and Fraser, C.M.
Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker

GI:12320593

AC069470.10

ACCESSION

VERSION

HTG; HTGS_PHASE1 thale cress.

ORGANISM

KEYWORDS SOURCE REFERENCE AUTHORS Submitted (01-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org on Jan 19, 2001 this sequence version replaced gi:12280790.

* NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

2 (bases 1 to 136047) Town,C.D. and Kaul,S. Direct Submission

REFERENCE AUTHORS TITLE JOURNAL

Unpublished

JOURNAL

TITLE

100163: contig of 100163 bp in length 100213: gap of unknown length 112623: contig of 12410 bp in length 112673: gap of unknown length 116686: contig of 3963 bp in length 116686: app of unknown length 116080: app of unknown length 136047: contig of 19361 bp in length.

be preserved

/organism="Arabidopsis thaliana"

Location/Qualifiers

source

FEATURES

/db_xref="taxon:3702" /chromosome="1"

clone-"IGF-F7F7"

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91210
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                                       1213 ATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTGGAGG 1272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796 CTTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGAAATCATTCACAGCAGATG 855
394 TCGAAGAATCCGATAGAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1036 AGATAAAAAAAGGATCAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGG
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                                                                                 454 GCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTC
                                                                                                                                                                     514 TCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACA - CATTGAAAATGAAGATGAAGA
                                                                                                                                                                                                                                                      572 TGAAGAATTTAAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATT
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                                                                                                     Length 136047;
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                                                                                                     Score 68.8; DB 74; Length
Pred. No. 6.1e-06;
0; Mismatches 507; Indels
  151 others
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46028 a 22872 c 22213 g 44783 t
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Best Local Similarity 46.3%;
Matches 461; Conservative
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AC069470 136047 bp DNA HTG 19-JAN-2001 Arabidopsis thaliana chromosome I clone IGF-F7F7, *** SEQUENCING IN

RESULT 14 AC069470/C LOCUS DEFINITION

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                                                     28495 AGGGACTCACCTCATCATCACTTCACTTGTCAACGTTGTTGTTGCCAACGG 28436
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                             765 TCCAGAGTTCCAAGTTTAGTCCATCTCTTTTTTTTGTAGCGATTGCAGCTTATATGTGG
                                                                                             825 GCTGGCATAACGAAATCATTCACAGCAGATGAAGACCAAGACAACGAGGATGCATTTTTC
                                                                                                                                                            TTGATTCCGGTCGATCTAAGGCCACGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGG
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    4.4%; Score 65.8; DB 10; Length 7
1 Similarity 7.5%; Pred. No. 2.1e-05;
31; Conservative 219; Mismatches 161; Indels
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Dorner,F., Schelfilinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                       ttttcacccaatccaaaattaagaaattgaagggttggattcagtccagagttccaagtt
                                                                                                                                   TAGTCCATCTCTCATCTTTTGTAGCGATTGCAGCTTATATGTGGGGCTGGCATAACGAAAT
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plants; acylation; colour; tone; colouration; colour change;
Gentiana triflora; Petunia hybrida; Perilla ocimoides;
Scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                                                                                                            Mizutani
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          /*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                                                            Kusumi T,
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                                                                                       ACCCCCGTCGTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants
                                                                                                                       Aromatic acyl transferase; transformation; anthocyanin pigment; plante; colourtation; colour change; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.7%; Score 216.8; DB 17; Length 1622; llarity 50.8%; Pred. No. 5.7e-47; Conservative 0; Mismatches 662; Indels 57;
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/product= Aromatic acyl transferase.
701..703
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/transl_except= AAT encodes Asp
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                                                                                                                                                                             triflora var. japonica (Clone pGAT106)
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Tanaka Y, Yonekura K;
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/transl_except= ATC encodes
1322..1324
                                                                                                    Aromatic acyl transferase coding sequence.
                                        BP.
                                      AAT37309 standard; cDNA to mRNA; 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 57-61; 94pp; Japanese.
                                                                                                                                                                                                 Location/Qualifiers
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95JP-0067159.
95JP-0196915.
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17-FEB-1995;
29-JUN-1995;
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Matches 741;
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981 CGAGAGCTGGTGGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGGGGAGATA 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATAGATCCGTCATAAAATATCCGACGAAATTTG-----ACTCCATTTATTGGAGAAAC 653
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                                                             123 GAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTCAAACAATCT
                                                                                                                          agattecgecateettgteecaae---tetaaatttateattteateeattaaategtee
                                                                                                                                                                                       CICTCIAAAACTCICAIACACTICTICCCICTCICAIGCAATTIAATCIACCCTTCA---
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tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl
                                         1259 gigcaigaittigaigcagaittiggitggggaaagcitgaaaagcaigaaicigittica
                                                                                                                                   ATTGATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTG
                                                                                                GAGGTTTGCTTGTCTTTGCCTAAGGACAAATGGATGCTTTTTGCTGCTTATTTTCACTG
                         CTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCG
                                                                                                                                                                                                                                                                                                          Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukui Y, Kusumi T, Mizutani
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/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                          Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 69-72; 94pp; Japanese.
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                                                                                                                                                                                                                                                                        (first entry)
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P-PSDB; AAW04726.
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17-FEB-1995;
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tone changes and allowing new colourations to be produced. Sis
specific DNA sequences encoding aromatic acyl transferase from
different plants are described in AAT37308-T37313.
                                                                                                                                                        Length 1508;
                                                                                                                                                                                            0; Mismatches 654; Indels
                                                                                             BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                      DB 17;
                                                                                                                                                                            3.9e-40;
                                                                                                                                                        Score 190.6;
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                                                                                                                                                                            Pred
                                                                                                                                                    12.9%;
                                                                                                                                                                                            Matches 676; Conservative
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                                                                                               Sequence 1508
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                                             tggtaactgtggtgcaccatgtgtcccgaccttaaaaaatgtcgttttgactagcgaaaa 1018
                                                                                                                                                                          GAAGGCGAGAAAGCAAGAAATATTGTCGATTGATGGGGAGAAATATGCAATGACGCTTTG 1240
                                                                                                                                                                                     TAAAGCCAGGGATTTCGAAGGAGTTTGGAGGTTTGCTTTGTCTTTGCCTAAGGACAAAAT 1300
                                                                                                                                                                                                                                tgcaagcaaaacatcagcacaagatcttgaaattggattgagtctaccgagtatgcaaat 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA coding for aromatic acyl transferase - for transforming plants
ggacggaatcttgaaagatgccgcgagatggcatga---acctttcatgatcccggctag
                                                                                                                                                        CGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGCGGCGAGAGCTGGTGGGGAGAGAA
                                                                                 1019 tgggtatgcacttggtgctaaagtaattggagagtctatatgcaaaatgatatataaa
                                                                                                   GAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATC
                                                                                                                                      1121 ATATITITCGGTGGCAGGATCGAGCAAGCTAGATCTTTACGGTGCAGATTTTGGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                       Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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                                                                                                                                                                                                                                                                   1313 ggaggcgttttctagcatctttgatgaaggattagagagtcaa 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gentiana triflora var. japonica (Clone pGAT4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kusumi
                                                                                                                                                                                                                                                                                                                                                                       Aromatic acyl transferase coding sequence.
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ura K;
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איבים M, Tanaka Y, Yonekura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95JP-0046534.
95JP-0067159.
95JP-0196915.
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                                                                                                                                                                                                                                                                                                                AAT37308 standard;
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                 with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                         Vectors containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 ATCTACCCTTCATCCCCGGAGAAATGCCGGAGTTTCGGTA-----TCTATCCGGGAC
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which produce anthocyanin pigments and thus altering colour tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 1703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 175.4; DB 17;
llarity 49.6%; Pred. No. 3.8e-36;
Conservative 0; Mismatches 666;
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us-08-894-356c-4.rng

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                                                                AGAATGCGGCGGCGAGAGCTGGTGGGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATC 1028
                                                                                                  GCGCCGGAGATAAAAAAAAGGAT --- CAACGACAAGAGAATATTAGAAACGGTGGAGAAA 1085
                                                                                                                                                                                          AAGCTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTG 1205
                                                                                                                                                                                                                                     1392 gaaggettttgetetttgteatagtetetttaatagaaceatatttgetgeaataagta 1451
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ggagaagccattgaaaagaggttgcacaacgaaaaaggcgttcttgcagatgcaaaaact
                                                                                                                                                                     TCGATTGATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGA
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                        -----ACCAAGACAACGAGGATGCATTTTTCTTGATTCCGGTCGATCTAAGGCCA
                                       gaatcatcgaacgaaaaatgagctcgagtacttcagttttacagcggattgccgagga
                                                        CGATTAGATCCGCCGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCG
                                                                                                                                                                                                                                                                                              CTGGGAATTAATGGTTAATGTATGTAATTAAACTAATTATTATTATGTAACAATTAA
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                                                                                                                                                                                                                                                                                                                                                                                       AAF58252 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1154 TCTTTACGGTGCAGATTTT3GATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCGATTGA 1213
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491
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                                                                                                                                                              The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1274 TTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 936;
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                                                                                                                                                                                                                                                                                                                                                               Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 6.4%; Score 94.8; DB 22;
1 Similarity 7.1%; Pred. No. 3.5e-15;
36; Conservative 284; Mismatches 186;
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                                                                                                         Example 6; Page 127; 159pp; English
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.4%; Score 94.8; DB 22; Length Best Local Similarity 7.1%; Pred. No. 3.5e-15; Matches 36; Conservative 284; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
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                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC.
                                                       26-JUL-2000; 2000WO-US20476
                                                                                    26-JUL-1999; 990S-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                                                                monitoring gene expression
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                                                                                                                                                                                                                                               single surface
WO200107665-A2
                            01-FEB-2001
                                                                                                                                                           Umek RM;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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llarity 7.1%; Pred. No. 3.5e-15;
Conservative 284; Mismatches 186;
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AAF58257/c
ID AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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                                                                                                                                         (first entry)
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Best Local Similarity
Matches 36; Conserv
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(CLIN-) CLINICAL MICRO SENSORS INC.
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2000US-0190259
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17-MAR-2000;
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1394 TGAGTAACGTGAAGAATAATCCCTATTATATTTATGATTTGGTTCAAATAAAGTGTAA 1453
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                                                                             1454 AGCCTCTTGAAAAAAAAAAAAAAA 1479
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                                                                                                 370 МИМИМИМИМИМИМИМИМИМИМИМ 345
                                                                                                                                                                                                                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC.
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2000US-0190259
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17-MAR-2000;
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1274 TTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTTATTTTCACTGGGAAT 1333
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TCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAGCAAGAATATTGTCGATTGA 1213
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 Length 936;
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 DB 22;
6.4%; Score 94.8; DB 22;
Llarity 7.1%; Pred. No. 3.5e-15;
Conservative 284; Mismatches 186;
                                                                                                                                                                                                                                                                           1454 AGCCTCTTGAAAAAAAAAAAAAAAA 1479
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17-MAR-2000; 2000US-0190259
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       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1094 GGAGATTCGTAAAGCGTTGCAGAAATCATATTTTTCGGTGGCAGGATCGAGCAAGCTAGA 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAGGAGGATTGGAGGT 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1394 TGAGTAACGTGAAGAATAATCCCTATTATATTATTATGATTTGGTTCAAATAAAGTGTAA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034 GGAGATAAAAAAAGGATCAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCC 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAATGGTTAATAAATGTATGŤAATTAAACTAATATTATTATGTAACAATTAATTAAGTGT 1393
                                                          The present invention relates to a composition comprising two nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 ИИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИТААССИМИМИМИМИМИМИМИМИМ 371
                                                                                   acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTTGCTGCTTATTTTCACTGGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                           Length 938;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 94.8; DB 22; ilarity 7.1%; Pred. No. 3.5e-15; Conservative 284; Mismatches 186;
                                                                                                                                                                                                                                                                       Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 AGCCTCTTGAAAAAAAAAAAAAAA 1479
Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 ИМИМИМИМИМИМИМИМИМИМИМИМ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200107665-A2
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ATTAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTATATATTTATGATTTGGTTC 1440
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иминичичистиничин иминичиничичичичичичичичичичичичичичичи 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781 TAGTCCATCTCTCATCTTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.4e-14;
00; Mismatches 305; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETM; mismatch; genotyping;
                                                                                                                                                                                         1441 AAATAAAGTGTAAAGCCTCTTGAAAAAAAAAAAAAA 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other
                                                                                                                                                                                                                                                   741 WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450;
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                                                                                                                                                                                                                                                                                                                                                                                                          AAF58254 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0145695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron-transfer group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide D1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF58254;
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Matches
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                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1321 TTTCACTGGGAATTAATGGTTAATAATGTATGTAATTAAACTAATATTATTATGTAACA 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTGCCGAGAATGCGGCGGCGGAGAGCTGGTGGGAGAGAAAGGGGTGTTTCTGGCAGCTG 1020
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llarity 0.5%; Pred. No. 3.4e-14;
Conservative 450; Mismatches 305; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English.
                                                                                                                                                         (CLIN-) CLINICAL MICRO SENSORS INC
      26-JUL-2000; 2000WO-US20476.
                                                            26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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Matches 4; Conserv
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                                                                                                                                                                                                                      Umek RM;
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                                                                                                                                                                                                  1021 AGGTAATCGCGGCGGAGATAAAAAAAGGATCAACGACAAGAGAATATTAGAAACGGTGG
                                                                                                                                                                                                                                                                                                                                   1081 AGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAATCATATTTTCGGTGGCAGGAT
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                                                                  381 wwwwwwwgcttawwwwwwwwwwwwwwwwwwwwww
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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gene expression; ss.
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AAF58257
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                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        721 TTTTCACCCAATCCAAAATTAAGAAATTGAAGGGTTGGATTCAGTCCAGAGTTCCAAGTT 780
                                                                                                                                                                                                                                                                                                                                                           781 TAGTCCATCTCTCATCTTTGTAGCGATTGCAGCTTATATGTGGGCTGGCATAACGAAAT 840
hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                                                                                                                                                                                ilarity 0.5%; Pred. No. 3.4e-14;
Conservative 450; Mismatches 305;
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Pred. No. 3.4e-14;
                                             Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                6.2%;
                                                                                                                                                        monitoring gene expression.
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                a single surface
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RESULT

us-08-894-356c-4.rng

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AGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATCATATTTTCGGTGGCAGGAT 1140
                                                            1141 CGAGCAAGCTAGATCTTTACGGTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAA 1200
                                                                                                                     1201 TATTGTCGATTGATGGGGAGAAATATGCAATGACGCTTTGTAAAGCCAGGGATTTCGAAG 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 936;
                                                                                                                                 Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                             (CLIN-) CLINICAL MICRO SENSORS INC.
                AAF58259 standard; DNA; 936 BP
                                                                                                                                                                                                                                                                    26-JUL-2000; 2000WO-US20476
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17-MAR-2000; 2000US-0190259
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                                                                          (first entry)
                                                                                                     Oligonucleotide D2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single surface
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                                                                          24-APR-2001
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                                                                                                                                                                                Synthetic.
                                            AAF58259;
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AAF58259
ID AAF5
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Search completed: November 5. 2001, 18:11:47
Job time: 15442 sec
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Best Local Similarity 0.5%; Pred. No. 3.4e-14;
Matches 4; Conservative 450; Mismatches 305; Indels
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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 288, App Sequence 1, Appli Sequence 2, Appli Sequence 5, Appli

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Sequence:

Searched:

Database

Result ò S

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COUNTER: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
US-08-242-677-1
US-08-446-855A-1
US-09-105-11
US-09-020-033-1
US-09-020-033-1
US-08-998-416-288
US-08-998-416-487
US-08-749-391-1
US-08-749-391-1
US-08-740-152A-3
US-08-740-152A-3
US-08-740-35B-1
US-08-740-152A-3
US-08-74-391-1
US-08-74-391-1
US-08-44-391-1
US-08-44-391-1
US-08-44-391-1
US-08-44-391-1
US-08-44-391-5
US-08-44-931-5
US-08-44-93-5
US-08-44-93-5
US-08-44-93-5
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. 5.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP 91 114 300.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                               ; Sequence 14, Application US/08232463
; Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30477
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149,
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
  51173
88920
18920
2061
2061
832
832
2058
2058
2058
2058
44483
4483
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US-08-232-463-14
  FILING DATE:
                                                                                                                                                                                                                                                                                                                    US-08-232-463-14/c
  RESULT
                                                                                                    (without alignments)
1659.305 Million cell updates/sec
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Sequence 186, App
Sequence 288, App
Sequence 6, Appli
Sequence 13, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 39, Appli
Sequence 39, Appli
Sequence 9, Appli
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Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Patent No. 520236
Patent No. 520236
Patent No. 520236
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Sequence 14, Appl
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Sequence 27, Appl
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                                                                                                                                                                   ; Search time 168.74 Seconds
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Sequence 1
Sequence 2
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-07-593-657-14
US-08-998-416-1187
US-08-998-416-288
US-08-998-416-288
US-08-998-416-288
US-08-998-416-28
US-08-998-416-28
US-08-916-43A-16
US-08-916-443A-16
US-08-916-443A-16
US-08-916-43A-16
US-08-915-593-39
US-08-915-593-39
US-08-916-288-8
US-08-918-918-9
US-08-918-918-9
US-08-918-918-9
US-08-918-918-9
US-08-918-918-9
US-08-918-918-9
US-08-918-918-9
                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
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US-08-913-842-27
US-08-913-842-1
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US-08-913-842-2
                                                                                                                                                                                                                                     324599 segs, 94655562 residues
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                                                                                        5, 2001, 18:04:28
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              nucleic search, using sw model
                                                                                                                                                                                             IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                         US-08-894-356C-4
1479
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Query
Match Length D
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                                                                                                              1505 AAAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTAAAAGAGATAGAA 1446
                                                                                                                                                                                     982 GAGAGCTGGTGGGAGAGAAAGGGGTGTTTCTGGCAGCTGAGGTAATCGCGGCGGAGATAA 1041
                                                                                                                                                                                                                                                                   1042 AAAAAAGGATCAACGACAAGAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTC 1101
                                                                                                                                                                                                                                                                                                                                           1102 GTAAAGCGTTGCAGAAATCATATTTTCGGTGGCAGGATCGAGCAAGCTAGATCTTTACG 1161
                                                                                                                                                                                                                                                                                                                                                                                                                      1162 GTGCAGATTTTGGATGGGGGAAGGCGAGAAAGCAAGAAATATTGTCGATTGATGGGGGAGA 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      922 CGGTTCCTGAAAATTACTTCGGGAACTGCTTATCGTACGCGCTGCCGAGAATGCGGCGGC 981
                                                                             862 AAGACAACGAGGATGCATTTTTTTTTTTTCGGTTCGATCTAAGGCCACGATTAGATCCGC 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.4%; Score 65.8; DB 1; Length 7218; 7.5%; Pred. No. 9.7e-10;
                                      31; Conservative 219; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLEOX VI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                      Best Local Similarity
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Query Match
                                      Matches
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INSECT-SPECIFIC PARALYTIC NEUROTOXIN
GENES FOR USE IN BIOLOGICAL INSECT CONTROL: METHODS AND
COMPOSITIONS
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                                                                                                                                                                                                                                                                                                               60 CCGCTCACATTCTTCGACATGACGTGGCTGCATTTTCATCCCATGCTTCAGCTCCTCTTC 119
                                                                                                                                                                                                                                                                                                                                                                                                      120 TACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTCAAAACAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 TCTCTCTCTAAAACTCTCATACACTTCTTCCCTCTCATGCAATTTAATCTACCCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 CTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAAACTCTTC
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                                                                                                                                                                                                                           Length 7218;
                                                                                                                                                                                                                         Query Match 3.9%; Score 57.2; DB 1; Length 7 Best Local Similarity 3.8%; Pred. No. 4.2e-07; Matches 14; Conservative 213; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/593,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/07593657; Patent No. 5266317; GENERL INFORMATION: APPLICANT: Tomalski, Michael D. APPLICANT: Miller, Lois K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                  LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19901004
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                ; CLONE: PTZ9pt-F1s
US-08-232-463-14
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                      linear
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                                                                                                           IMMEDIATE SOURCE
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                                                                                        TOPOLOGY:
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: 615 base pairs
nucleic acid
EDNESS: single
  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (96
ORIGINAL SOURCE:
ORGANISM: PAG1074RP
US-08-998-416-186
                                            TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1476 AAAA 1479
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                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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APPLICANT: Philippsen, Rainer
APPLICANT: Sebles
APPLICANT: Sebles
APPLICANT: Sebles
APPLICANT: Mendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Record ADDRESS: 1152
CORRESPONDENCE ADDRESS: 1152
CORRESPONDENCE NO. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                  Query Match 2.9%; Score 42.6; DB 1; Length 319; Best Local Similarity 52.5%; Pred. No. 0.0016; Matches 93; Conservative 0; Mismatches 84; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY, AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 186, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                             TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: GOUDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
TELEFAX: 303/499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: CDNA to mRNA

US-07-593-657-14
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.
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US-08-998-416-186
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1356 ATTAAACTAATATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCC 1415
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APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                     Query Match 2.8%; Score 41.6; DB 4; Length 615; Best Local Similarity 51.6%; Pred. No. 0.0049; Matches 95; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 4-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER. PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1137, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
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Pohlmann, Rainer
Steiner, Sabine
DNA (genomic)
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919-541-8689
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US-08-998-416-288
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       TELEFAX:
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                                                                                                                                                                                                                                                                                          1356 ATTAAACTAATATTATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCC 1415
                                                                                                                                                                                                                                                                                                                                                                                    7 AATATATATATATATATAAAGATTAATATATAAACCTTTTTTATAAATATTTAAGTA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Philippsen, Peter
APPLICANT: Pollmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Wondry Christine
APPLICANT: Wondry Unistine
APPLICANT: Wenchland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 622000
                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                       Score 41.6; DB 4; Length 636;
Pred. No. 0.0051;
0; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUSTREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
       1137:
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                       2.8%;
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 636 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                   Query Match 2.8
Best Local Similarity 51.6
Matches 95; Conservative
                                                                                                                                              ; ORGANISM: PAG1692RP
US-08-998-416-1137
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US-08-998-416-288
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GENERAL INFORMATION:
APPLICANT: Tomalski, Michael D.
APPLICANT: Miller, Lois K.
TITLE OF INVENTION: INSECT-SPECIFIC PARALYTIC NEUROTOXIN
TITLE OF INVENTION: GENES FOR USE IN BIOLOGICAL INSECT CONTROL: METHODS AND
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                  1356 ATTAAACTAATATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCC 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                       Length 837;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       Score 41.6; DB 4;
Pred. No. 0.0061;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Greenlee and Winner, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/07/593,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Sequence 6, Application US/07593657
: Patent No. 5266317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                         2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         Query Match 2.8
Best Local Similarity 51.6
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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FILING DATE: 19901004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                            PAG1241RP
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CLASSIFICATION: 435
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OPERATING SYSTEM:
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin.zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1391 TGTTGAGTAACGTGAAGAATAATCCCTATTATATATTTATGATTTGGTTCAAATAAAGTG 1450
   Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.6; DB
Pred. No. 0.41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 15628 AAAATGATTATAAAAAAAAT.\AAAAACAAA 15656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy cisk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-916-443A-16
Sequence 16, Application US/08916443A
; Patent No. 6001986
                                                                                                                                                     ; Sequence 13, Application US/08487826B
; Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (619) 235-3550
TELEFAX: (619) 235-0176
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               Patent No. Journal APPLICANT: Sim, Kim L. APPLICANT: Sim, Kim L. APPLICANT: Chitnis, Chetan APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.6%;
ilarity 53.7%;
Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Ma
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COMPUTER READABLE FORM:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 80; Conserva
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US-08-487-8268-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                           RESULT 9
US-08-487-826B-13
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Patent No. 62352B
Patent No. 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1056 atttttaaattagtaaaatttcgataattttacttaatttttaaattttactaaattgac 1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1363 TAATATTATGTAACAATTAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1363 TAATATTATTATGTAACAATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTAT 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39.4; DB 1; Length 1241; Pred. No. 0.037; 0; Mismatches 86; Indels 0
                                MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.7%;
Best Local Similarity 51.4%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Ver. 2.0
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-103..-100
                                                                                           CDS
119..985
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; LOCATION: (119)..(985)
US-08-942-0128-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                 unsure
47..49
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SEQ ID NO 3
LENGTH: 1241
                                                                                                                                                                                  NAME/KEY:
LOCATION:
TOPOLOGY:
                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-07-593-657-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-942-012B-3
                                                                                                                        LOCATION:
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                                                          FEATURE
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3: Naval Medical R & D Command
Bldg 1, T-12, 8901 Wisconsin Avenue
Naval Medical
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STREET: Two ...
CITY: Lexington
..me: Massachusetts
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; Patent No. 5912140 5776726
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                                                                          COUNTRY: U.S.A
ZIP: 20889-5606
                                                            Maryland
                      STREET: Bldg 1
CITY: Bethesda
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                              TITLE OF INVENTION: Antiviral Proteins, Amarandin 1 and 2, from TITLE OF INVENTION: Amaranthus Viridis, DNAs Encoding Therefrom NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 36.4; DB 3; Length 1116; 55.6%; Pred. No. 0.29;
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Patent No. 5814617
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Hoffman, Richard C.
APPLICANT: Hofstrom, Richard C.
APPLICANT: Dollan, Denise L.
TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WORDPEFIECT 6.1 Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFRENCE/DOCKET NUMBER: 1942/18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/916,443A FILING DATE: 22 AUG 1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1116 nucleic acids
                                APPLICANT: Sun Chung PARK APPLICANT: Soo Kyung OH APPLICANT: Hosull LEE APPLICANT: Jeong Woo CHO APPLICANT: Chang H. CHUNG
                Yong Sig KIM
Sun Chung PARK
Soo Kyung OH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: genomic DNA
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Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Flopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                        USA
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US-08-319-704-5
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1265 ATTGGAGGTTTGCTTGTCTTTGCCTAAGGACAAAATGGATGCTTTTGCTGCTGCTTATTTTC 1324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1385 ATTAAGTGTTGAGTAACGTGAAGAATAATCCCTATTATATATTTATGATTTGGTTCAAAT 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Whoriskey, Susan K.
APPLICANT: Whoriskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Too, Niajun
APPLICANT: Schimmel, Paul R.
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: Synthetase Genes, Tester Strains and Assays NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1422;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.4; DB 1;
Pred. No. 0.34;
0; Mismatches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 CAATTATAATCCAATATAAGCATATAATTTAAGA 328
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: A. David Spevack
REGISTRATION NUMBER: 24,74
REFERENCE/DOCKET NUMBER: 75,206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-4022
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,704
FILLIG DATE: 07-00T-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/08415593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic)
US-08-319-704-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 48.1%;
Matches 103; Conservative 0
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LENGTH: 1422 base pairs
TYPE: nucleic acid
STRANDEDNESS': single
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1274 TIGCTIGICITIGCCIAAGGACAAATGGATGCTTTTGCTGCTATTTTTCACTGGGAAT 1333
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APPLICANT: PYTO, Anna M.
TITLE OF INVENTION: MUCIPLE COMPONENT RNA CATALYSTS AND TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Score 36.4; DB 2; Length 2.48.5%; Pred. No. 0.45; tive 0; Mismatches 106; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/378,235B
FILING DATE: 25-JAN-1995
FILING DATE: 25-JAN-1995
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Cooper and Dunham, LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 AGCCTCTTGAAAAAAAAAAAAAAAA 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-415-593-39
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                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BLOCK, DAVID E.
REGISTRATION NUMBER: 22.592
REFERENCE/DOCKET NUMBER: CPI9-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAN: 617-862-9540
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2128 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 100; Conservative
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STATE: New York
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APPLICANT: Whorlskey, Susan K.
APPLICANT: Quinn, Cheryl L.
APPLICANT: Too, Niajun
APPLICANT: Too, Niajun
APPLICANT: Schimmel, Paul R.
TILE OF INVENTION: Synthetase Genes, Tester Strains and Assays NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1991;
                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,593
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2.5%; Score 36.4; DB 2;
Best Local Similarity 48.5%; Pred. No. 0.43;
Matches 100; Conservative 0; Mismatches 106;
                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTONEJAGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
RECERENCEJOCKET NUMBER: CP194-09
TELECHOME: 617-861-6240
TELEFAX: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1454 AGCCTCTTGAAAAAAAAAAAAAA 1479
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Patent No. 5912140
Patent No. 5912140 5776726
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-862-9540
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1991 base pairs
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CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION: 29..1780
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US-08-415-593-40
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US-08-415-593-39
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              Query Match 2.4%; Score 36; DB 2; Length 174; Best Local Similarity 58.3%; Pred. No. 0.11; Matches 63; Conservative 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/COCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-310
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                    28,678
ER: 0575/45553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/867,106 FILING DATE: 19920625 PRIOR APPLICATION DATA: APPLICATION NUMBER: AU PJ 7187 APPLICATION NUMBER: PCT/AU90/00530 FILING DATE: 02-NOV-1989 ATTORNEX/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPAN: 212-278-0400
TELEPAN: 212-991-0525
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-378-235B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                               LENGTH: 174 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-07-867-106-2
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                                                                                                                            Length 5852;
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Pred. No. 1.2;
0; Mismatches 120; Indels
                                                                                                                           Query Match 2.4%;
Best Local Similarity 47.4%;
Matches 108; Conservative
                        CDS
2378..5038
                                                             CDS
2378..5038
                        NAME/KEY:
LOCATION:
ANTI-SENSE:
FEATURE:
                                                              NAME/KEY:
                                                                          ; LOCATION:
US-07-867-106-2
                                                 FEATURE:
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Search completed: November 5, 2001, 18:04:45 Job time: 15085 sec

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(without alignments)
2403.520 Million cell updates/sec
                                                                                                                    November 5, 2001, 18:00:51 ; Search time 5816.79 Seconds
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Listing first 45 summaries
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em_esthum8:*
em_esthum9:*
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_inv4:*
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em_gss_rod8:*
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AUTHORS
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AW221049
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KEYWORDS
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1 (bases 1 to 690)

van der Hoeven, R., Bezzeridaes, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes Unpublished (2000)

Contact: Cathy Ronning

The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries Division tell.800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG599447 690 bp mRNA EST 12-APR-2001
EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                 492
ATATICCAIGGITCTACTGCCACCCCATCCACGCATCTTCTTCTATGACTTTCCCCACC 196
                                                                                                                                                                                                                                                                                  CTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAAC---TCTTCCAAGTTTTCGCCG 432
                                                                                                                                                                                                                                                                                                                                                                                                             TTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACA 552
                                             CCACATACGCTACCTTGATGGAGACTCTCTCTCTTCACCGTTGCAGAGTCCACCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         617 AAGGAAACATGGCTINNCTTTCAACCTCTNTGTCTTTTTTTTTTTTTAAGAGGGACAAAG
                               TCATACACTICITCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCGGAGAAAATGC
                                                                                                                                                         CGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="grouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar-"Kennebec"
/db_xref-"taxon:4113"
/clone-"cSTS25122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="cSTS"
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Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BG599447
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TTAAAGATCC 686
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XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit mature green, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAATTCACTCTCCCCTCACT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCCGGAGAAATG 254
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Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTT
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                                                                                                                                                                                                                          Score 131.8; DB 155; Lengt
Pred. No. 2.2e-23;
0; Mismatches 262; Indels
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546 GGAGATGAACA 556
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                                                                                                                                                                                  /crganism="Lycopersicon esculentum"
/cultivar="TA496"
/dultivar="TA496"
/dultivar="TA496"
/dultivar="TA496"
/dultivar="Laxon:4081"
/clone="Laxon:4081"
/clone="Laxon:4081"
/clone="Lib="tomato fruit mature green, TAMU"
/clone="Lib="tomato fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/dev_stage="mature green (3-5 days pre-ripening)"
/dot="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; cLEF - Fruit were tagged at the low stage and
harvested 3-5 days prior to ripening. Eruit were cut in
half to verify the seeds were indeed 'immature' and the
seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 113; Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.9%; Score 131.4; DB 113; Lengt
Best Local Similarity 52.0%; Pred. No. 2.8e-23;
Matches 294; Conservative 0; Mismatches 271; Indels
            Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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                                                                                                                                     prime sequence.
Location/Qualifiers
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/tissue_itype="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR" ste_1: EcoRI: Site_2:
/note="vector: pBluescript Sr.; site_1: EcoRI: Site_2:
XhoI: CDNA was prepared from poly4+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Glapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                   Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
1 (bases 1 to 783)
1 10 783)
1 Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J.
and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                              ESTS from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
Glomus versiforme, 2001
Unpublished (2001)
Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 CCGCTCACATTCTTCGACATGACGTGCTGCATTTTCATCCCATGCTTCAGCTCCTCTT 119
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BG584708 783 bp mRNA EST 11-APR-2001
EST486469 MHAM Medicago truncatula/Glomus versiforme mixed ES'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mjharrison@noble.org
Noble EST name: N380179e TIGR sequence name: MTDBT67TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

8.8%; Score 130.8; DB 155; Length 783;
Best Local Similarity 53.3%; Pred. No. 4.2e-23;
Matches 323; Conservative 0; Mismatches 277; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
                                                                       library cDNA clone pMHAM-19K14 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"pMHAM-19K14"
/clone_lib-"MHAM"
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Similarity
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              Best Local Sim
Matches 282;
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
(bases I to 570)
van der Hoeven, S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE922784 570 bp mRNA EST 02-0CT-2000 EST426553 potato leaves and petioles Solanum tuberosum cDNA clone cSTB22E2 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                     249 AATTCCCAAAACACCGATCCTTACATACGTTACCTCGATGAAGACTCTATCTCCTTCACC 308
                                                                               ATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTT 356
                                                                                                                                                                                   369 IGGCACCATCITGITCCAAATTTACCICCACCTCGTACCGAACAAGACAACACTCGCATC 428
                                                                                                                                                                                                                                                                                                                                                                               AGTTACAACCATGTTGCTGCAGACGGAAAATCACTTCACCATTTCGTGAAATTTTGGCCC
                                                                                                                                                                                                                                                                                                                                                        TCAATGAGCAAACACTTGAAAATGAAGATGAAGATGAAGAATTTAAAATCTTTGCCAGTT
            417 TTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATA
                                                                                                                                                                                                                                                                                        GCAACGCATCACACCGTTAGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCT
                                                                                                                                                 357 AGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB22E2"
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1 (bases I to 583)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
kukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW221050 583 bp mRNA EST 07-DEC-1999 EST297519 tomato fruit mature green, TAMU Lycopersicon esculentum CONA clone CLEF3F3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                               CGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGTGTATCCATTGGTTTCAT 510
                                                                                                                                                                                                                             121 ACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTCAAAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                              181 CTCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAACTCTTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AAGTITICGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAA 480
                                                                                                                                                                                                    CGCTCACATTCTTCGACATGACGTGGCTGCATTTTCATCCCATGCTTCAGCTCCTTCT 120
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                                                                                                                           1 CCGTGATCGAAACGIGTAGAGTTGGGCCGCCGCCGGACTCGGTGGCGGAGCAATCGGTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 CGCATCACACCGTTAGCGACGCCCCGTTGTCTCGCGTTTATAACGGCTTGGTCT 536
  Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Lycopersicon esculentum"/cultivar="TA496"
     DB 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
  Score 129.6; DE
Pred. No. 8e-23;
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
8.8%;
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                                                    Conservative
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Query Match Best Local 9

Matches

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BASE CO ORIGIN

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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporanja'ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection, NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                   l (bases 1 to 763).
Zhang, P., Hernandez, M., Tornqvist, C.-E, Wirtz, U., Loukolanov, A.,
Rangel, P., Haberlach, G.T., Cho, J., Chiemingo, A., Bougri, O., Buell
C.R., Ronning, C.M., Heigeson, J. and Baker, B.
Infestans, Incompetible Reaction
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CTCAAACACTACACGCCCTTÄGCAGGAAATGTTGCTCGTCCACTAGATACAAATGGATAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTACAAGCTCCCCATT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 GACATGACGTGGCTGCATTT%CATCCCATGCTTCAGCTCCTTCTTCTACGAATTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GTAGAGTTGGGCCGCCGCCGCAC-TCGGTGGCGGAGCAATCGGTGCCGCTCACATTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 CTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCCGGAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGAC
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             Asteridae; euasterids I; Solanales; Solanaceae; Solanum
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es 257; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="p. infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="50kR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism "Solanum tuberosum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127.8;
Pred. No. 2.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar "Kennebec"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.6%;
Best Local Similarity 53.2%;
Matches 293; Conservative
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                                              REFERENCE
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/db_xref="taxon:4081"
/clone="tclEFP3"
/clone="tclEFP3"
/clone=lb="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/dev_stage="anture green (3-5 days pre-ripening)"
/lab_host="sOLR"
/lab_host="sol
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EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone
BPLI10A14 5' sequence, mRNA sequence.
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Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 CTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGATATTATTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 127.8; DB 113; Lengt
Pred. No. 2.3e-22;
0; Mismatches 272; Indels
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BG591758.1 GI:13609898
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al Similarity 51.7%;
291; Conservative
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267
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1 (bases 1 to 508)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, Generation of ESTs from potato leaves and petioles
Unpublished (2000)
                                                                                                                                                                                                       BG097054 508 bp mRNA EST 29-JAN-2001
EST461573 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB45p9 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 ACACCCTTAGCTGGCAACATTGCTTGTCGAGTTGATTTCGTGAGTTGCTT 262
                                  482 GGTGATGGAGCTACCATAGTAGGGTTCATTAAGGCGTGGGCTCTACTCCATAAATTCGGT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 CTGCATTTTCATCCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACAT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 ITTICAGAATCCATCGTTCCAAAACTCAAACAATCTCTCTAAAACTCTCATACACTTC 206
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                495 AGCGACGCCCCGTCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATT 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Rouning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
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Pred. No. 6.9e-20;
0; Mismatches 223; Indels
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/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB45P9"
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KEYWORDS
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/note-"vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
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(bases 1 to 564)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE921494 564 bp mRNA EST 02-OCT-2000
EST425179 potato leaves and petioles Solanum tuberosum cDNA clone
cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                          446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdnafresgen.com.
Location/Qualifiers
                                        46 CCTCCCCACGGGGGGCGAACAGAGCTAACGCTCCCTCTAACTTTTGATCATATGG 105
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                                                                                                                                                      TATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGAT 326
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                                                                                                                          CTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCG
                                                                                                                                                                                                                                              CCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTT
                                                                                                                                                                                                                                                                             TTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACG 501
                                                                                                                                                                                                                                                                                                                                                                                                    Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .564
/organism="solanum tuberosum"
/cultivar="kennebec"
/cultivar="taxon:4113"
/clone="csrB13B18"
/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 142;
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Pred. No. 2.2e-18;
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Similarity 52.3%;
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Medicago truncatula
Sukaryota, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I, Fabales, Fabaceae, Papillonoldeae, Medicago.
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VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, I
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447 TTCCCAGGCCGAGGCGT---CGGTATTGGAATAGCAACGCATCACCGTTAGCGACGCC 503
                                                                     CTGCATTTTCATCCCATGCTTCAGCTCTTCTACGAATTCCCTTGTTCCAAGCAACAT 146
                                                                                                                                                                                                                                                         132 TICGTICAAACCATTATICC?ACTCTTAAACATICACTCTCCCTCACTCTCAAAACATCTAC
                                                                                                                                                                                                                                                                                                                          207 ITCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCGGAGAAAATGCCGGAGTTTCGG 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCGAATCTTGGCATATCCCGTTGGTGTTTAGTAACCCATCATGTCGCTTGTGATGGA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE187619 788 bp mRNA EST 22-JUN-2000
EST336180 KVO Medicago truncatula CDNA clone pKV0-1613, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTs from uninoculated seedling roots of Medicago truncatula
                                                                                                                                                              172 TTCGTTTTGGCTATATGCGCGGATTTATTCTACAAGCTACCAATTTCCAAACTCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATGTGACTGGAGATTCTATATCTTTTATTGAGACTGATATGAATTTCAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 CCGTCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAA
                                             CCGCCGCCGCACTCGGTGCCGGAGCAATCGGTGCCGCTCACATTCTTCGACATGACGTGG
                                                                                                                                                                                                                                 292 ACACCCTTAGCTGGCAACAT%GCTTGTCCACTAAATTCGAGTGGTTATCCTGAGTTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTT
  Mismatches 251; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Kate@mail.b:o.tamu.edu
Texas A&W University name:T260795e
TIGR Sequence name:MTGAU50TK
More information is available at.
http://chrysie.tamu.edu/medicago
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Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE187619
BE187619.1 GI:8666803
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Texas A&M University
  Conservative
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  Matches 287;
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AUTHORS
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JOURNAL
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

I (bases 1 to 659)

S van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,

Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generations of ESTs from sprouting potato eyes

L Unpublished (2000)

Contect: Cathy Ronning

The Institute for Genomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI: Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG598154 659 bp mRNA EST 12-APR-2001
SET496832 CSTS Solanum tuberosum CDNA clone CSTS20M23 5' sequence,
mRNA sequence.
BG598154
                                                                                                                                                                                                            345
                                                                                                                                                                                                                                                                                                                                                446
                                                                                                                                                            326
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACGGTTAGCGACGCCCCG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 ACACCCTTAGCTGGCAACATTGCTTGTCCACTAAATTCGAGTTGTTATCCTGAGTTGCGT
                                                                                                                                                            TATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGAT
                                                                                                                                                                                                         TATGTGACTGGAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTCAATCAT
                                                                                                                                                                                                                                                         CTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCG
                                                                                                                                                                                                                                                                                                                                                  CCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTT
                                                                                                                                                                                                                                                                                                                                                                            207 TTCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCGGGAGAAATGCCGGAGTTTCGG
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Pred. No. 2.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 TCGTTTCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 ACCATCGTGAAATTCATAAGAACATGGGGTTTACTCAACAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS20M23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="cSTS"
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163 c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potato.
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DEFINITION

ACCESSION

ORGANISM

VERSION KEYWORDS SOURCE

RESULT 10

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BG598154

JOURNAL

TITLE

FEATURES

AUTHORS

REFERENCE

BASE COUNT ORIGIN

446

531

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Best Local Sim
Matches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                  source
                                DEFINITION
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JOURNAL
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                                                                ACCESSION
                                                                              VERSION
KEYWORDS
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                                                                                                                                                                                                                 AUTHORS
 BE922746
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                                                                                                                                                                                         Anote—"Vector: DBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Strategene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
from the rand propagated in XLOLR cells."
188 c 100 g 262 t lothers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 CICITCTACGAATTCCCTTGTTCCAAGCAACATTTTTCAGAATCCATCGTTCCAAAACTC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 AAACAATCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTAC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCC 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGTTCCCTTTGTTAGCTATTCAAATAACATCATTCCCAAATTATGGCTTTTCCATTGGC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTATGATCGAAGTGTGATTATCGACACAAATGACCTTCACGAAGTTTTCTTGAAAGAT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 CTAGCTTTTCATCATGTTGTTGCTGATGGAAGAACCTTCCACAATTTCATCAAAACATGG
                                                                                                                             /tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host-"E.coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACAATCTCTTTCTCTCACACTTCAACATTACTTCCCATTTTC----CGGTACATTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ACGGTCGCAGAGTCAAATAGCGACTTTGAACACTTGTGCTCCGATTACTCAAGAGATGTT
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                                                                                                                                                                                                                                                                                                                                                                          Score 109.8; DB 164; Length 788;
Pred. No. 1.1e-17;
0; Mismatches 292; Indels 6;
primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
                                        /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV0-1613"
                                                                                                              /clone_lib="KV0"
                                                                                                                                                                                                                                                                                                                                                                            Similarity 51.18;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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ORIGIN
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RESULT

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               EST426515 potato leaves and petioles Solanum tuberosum cDNA clone
STB21L12 5' sequence, mRNA sequence.
BE922746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 CTTAGCTGGCAACATTGCTTGTCCACTAAATTCGAGTGGTTATCCTGAGTTGCGTTATGT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 TGGTAACCATCCTCGAAAT---GCTAAGGATTTTTATCCCATTCCTCAATTGGCACAACC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 TAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACACTTTTTTC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GAATCTTGGCATATCCGTTGGTTTTAGTAACCATCATGTCGCTTGTGATGGAAATACCAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 TTTTCATCCCATGCTTCAGCTCCTCTTCTACGAATTCCCTTGTTCCAAGCAACATTTTTC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 ATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGAAATCGTCCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCAT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACGCCCCGTCGTT 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TCTCTCATGCAATTTAATCTACCCTTCATCCCGGAGAAAATGCCGGAGTTTCGGTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 TGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and petioles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 108; DB 142;
52.2%; Pred. No. 3e-17;
Live 0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 574
/organism="Solanum tuberosum"
/cultivar="Rennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cSTB21L12"
/clone_lib="potato leaves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4113"
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 9
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                                                                              BE922746.1 GI:10448822
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5 prime sequence.
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JOURNAL
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ORIGIN
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BE434257
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S van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTS from tomato nutrient-deficient roots
Unpublished (1999)
Context: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescriptSKmcUadapt; Site_1: 5' EcoRI;
Site_2: 3' KhoI: Roots were harvested from plants grown
under the following deficiencies/stresses: 10 mM Al, Zn,
P, K, Fe,N. mRNA was isolated from indivdual treatments.
Proportional aliquots of mRNA of each treatment were mixed
and used for library construction."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liang, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                       BF096979 482 bp mRNA EST 19-OCT-2000 EST400516 tomato nutrient deficient roots Lycopersicon esculentum CDNA clone CLEW18020 5' sequence, mRNA sequence.
512 TCTCGCGTTTATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGA 571
                                                                                         GACATGACGTGGCTGCATTTTCATCCCATGCTTCAGCTCCTCTTCTAGGAATTCCCTTGT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GACCATGTTGGTTAGGGTTTCGCCGTATGAGGCGGATATTATACAAGCTCTCCATT 123
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                    TGAAGAATTTAAAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCCGACGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="tomato nutrient deficient roots"
/tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_nost="SOLR"
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/cultivar="TA492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.2%; Score 106.6; DB 144, Best Local Similarity 51.6%; Pred. No. 6.7e-17; Matches 244; Conservative 0; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: dfrisch@CLEMSON.EDU.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="cLEW18020
                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                   BF096979.1 GI:10902689
                                                                                                                                             632 TGACTCCATTTATTGG 647
                                                                                                                                                                             537 AGGGACGATTATATGG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon.
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                                                                                                                                                                                                                                                                                        DEFINITION
                                                                      572
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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/note-"Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 591)
Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 24-JUL-2000 EST 24-JUL-2000 EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG15H6, mRNA sequence.

BE434257 GI:9432100
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Ebkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                          304 AATTTCAATTATCTCATTG5TGACCATCCGCGTAAGGCTATTTTTATCACTTG5T 363
                                                                                                                                                                                                                                                                                                                                  244 CCTGAGTTACGTTATGTGACAGGAGATTCTGTGTCTGTTACTTTTTCGAGACTGATATG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 CCTAAGTTAGGGGAACCTAAGGATGCACCGGGGGTCCAACTAGCCCCGCTCTTAGCCATT 423
CTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCATCCCCGGAGAAATG
                                                                                                                                                                                                                                                                  CCGGAGTTTCGGTATCTATCCGGGGACTCGGTTTCTTTCACCATCGCAGAATCTAGCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTAAATTGCCGCCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation of ESTs from tomato fruit tissue, breaker stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGTGACTCTTTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 CAGGIGACACITITICCGAMICITIGGIGIATCCATIGGITICACIAACCATCA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="tomato breaker fruit, TiGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .591
/organism:"Lycopersicon esculentum"
/cultivar:"74496"
/db_xref="taxon:4081"
/clone="cl.EG15H6"
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Tel: 864 656 4366
Fax: 864 656 4293
Emall: dfrischecLEMSON.EDU
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Clemson University
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Contact: David Frisch
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Search completed: November
Job time: 14896 sec
                                                                                                                                                          BASE COUNT
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1 (bases 1 to 487)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
van der Hoeven, R.S., Bezzeredes, J.L., Ronning, C.M., Nierman, W.,
F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon hirsutum estreptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW616206 487 bp mRNA EST 24-MAR-2000 EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHTID15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                              CCGCGTAAGGCTAAGGATTTTTATCACTTTGTTCCTAAGTTAGGGGAACCTAAGGATGCA 306
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                                                                                                                                                                                                                                                                                                                CCAGAATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAA 401
                                  Gaps
                                                                                      7 ATGAGGGGGATATTATTACAAGCTCTCCATTTCAAACCCGATTTCGTTCAAAACATT
                                                                                                                          402 TCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCTTTTCCCAGGCCGAGGC
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                                                                                                                                                                                      TCGGTTTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 ATAACGGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGT
 591;
                                ä;
   Length
Score 106.6; DB 167; Lengt
Pred. No. 7e-17;
0; Mismatches 249; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 AAATCTTTGCCAGTTTTCGATAGATCCGTCATAAAATATCC 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prime sequence.
Location/Qualifiers
1. 487
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AW616206.1 GI:7322240
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Contact: David Frisch
7.2%;
ilarity 51.6%;
Conservative
                Best Local Similarity
Matches 269; Conserv
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   Query Match
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VERSION
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/organism="Lycopersicon hirsutum"
/db_xref="taxon:62890"
/dlone="CLHTID15"
/clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/dev_stage="mixed stages"
/dev_stage="mixed stages"
/dev_stage: percent of trichomes. This procedure yielded a mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TATGCCCTTAGCCGGAAACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTACG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TTATGTGACAGGAGATTCTGTGTCTGTTAATTTTTCTGAGACTGATATGATTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCATTGTCGAAGAATCCGATAGAAAACTCTTCCAAGTTTTCGCCGTGCAGGTGACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCCCAGGCCGAGGCGTCGGTATTGGAATAGCAACGCATCACACCGTTAGCGACG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104.8; DB 118; Length 487;
Pred. No. 2e-16;
0; Mismatches 232; Indels 0;
                                                                                                                                                                                                                                                                                                                              163
                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%;
Best Local Similarity 51.3%;
Matches 244; Conservative (
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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E12753
AB029340
E12756
E12754
AB026494
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gb_htg25:"
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em_ph:*
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gb_in4:*
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2619.394 Million cell updates/sec
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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E12757 Senecio cru AB010708 Gentiana E12753 Gentianatri AB029340 Perilla oci E12756 Perilla oci E12754 Gentianatri AB026494 Gentiana

Description

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420
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                                                                                                                                                                                                                                                          1 TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTCGT
                                                                                                                                                                                                                                                                         1 TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGCCCATCGCTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 TATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGGTTCAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 CTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAAATAAGTTGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGATAAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTCTTAACCC
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                                                                                                                                                                                                                              4; Indels
                    /organism='Senecio cruentus
                                                                          'product-'acyltransferase'
                                 /tissue_type='petal'
/clone='pCAT48'
1.1367
                                                                                                                                                                                                 Score 1501.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                              477
                                                                                                1. .1508
/organism="unidentified"
/db_xref="taxon:32644"
                                                                                        Location/Qualifiers
                                                                                                                                             296 g
                                                                                                                                                                                                 Query Match
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KARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
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TEATE A LON- "MEDIOWIKULEKCOVTPPSDTTDVELSLPVTFFDIPWLHLNKWO SLLFVDFPF RRTHFLJOTVIPWLKASLSLTLKHTVPLGSGULLMPIKSGEMPKFOYSRDE GDSITLLIVAESDODFDTVIPWLKASLSLTLKHTVPLGSGULLMPIKSGEMPKFOYSRDE GDSITLIVAESDODFDTVIPWLGGOLLDMPIKTRORDDLLANULDSPUNTPWAOVTV FPNRGIAVALTANALTANERGODLLANLLDSFDRSIIKDV FPNRGIAVALTANERGODLLANLLDSFDRSIIKDL RGLEFFWNEWODVLEMFSREGSKPPRFNKYRATVLSLAGICKLKNKVLNIRGSEPTIKTTFFTATOKTVATKSKDDVYSESSNDENELEYFSFTADCRGLLTPPGPPNYFGNGLACYATHRELVGDKGLLLVANAAIGERIEKRHHNEKOVLADAKTWLSESNGIPSKREGITGSPREDGSRGVBLTSVDXAELIXVIGSSREGSEDITGSSPREDGSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSSRGVBLTGSSPREDGSSPREDGSSRGVBLTGSSPREDGSSPREDGSSRGVBLTGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSPREDGSSP
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Fukuchi-Mizutani,M., Nakao,M., Fukui,Y., Yamaguchi,M., Ashikari,T.
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                                                                                 cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora pplant J. 16 (4), 421-431 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
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/product="Anthocyanin 5-aromatic acyltransferase"
/protein_id="BAA74428.1"
/db_xref="GI:4185599"
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Pred. No. 1.5e-34;
0; Mismatches 616;
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/db_xref="taxon:55190"
/clone="pGAT4"
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                                             and Kusumi, T.
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                                                        647 AAATAAGTIGAGACATACAAG----GCTCGAAAGTITITATAAACCTICGAGCCTIGIIG 702
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GTCCCACTGATAAAGTTCGGTCAACGTTTGTGTTGACCCGGAACTAATATCAATACTAA
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Ashikari,T., Tanaka Y., Fujiwara,H., Nakao,M., Fukul,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T. .
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JP 1997070290-A/1.
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FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                                                                                                                                                                      ... L/-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915 PI 6715HIKAZU, FUJIWARA HIROYUKI, PI NAMASAHIRO, PI FUJIWARA HIROYUKI, PI PI FUKUI YUKO VANDONINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTAT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 AGGCCTCTTTGTCTCTCACTCTAAAACACTACGTTCCGCTTAGCGGAAATTTGTTGATGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 TICCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TATGTGATTGCGTCACGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 CGGGTATATCACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCA---TCGGCCATCGCT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 202.4; DB 10; Length 1703; 52.0%; Pred. No. 1.5e-34; tive 0; Mismatches 616; Indels 48;
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATCHT: JP 1997070290-A 1 18-MAR-1997;
SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism='Gentianatriflora'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product='acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product-'acyltransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /variety='japonica'/tissue_type='petal
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/db_xref="taxon:32644"
350 c 359 g 482
                                                                                                                                              18-MAR-1997
30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        (C12N9/10,C12R1:19);
strandedness: Double;
                                                                                               Gentianatriflora
JP 1997070290-A/1
                                                                                                                                                                                                                                                                                                                                                                                                               topology: Linear;
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/translation="VietCRVGPPPDSVAEQSVPLTFFDWTWLHFHPMLQLLFYEFPC
SKQHEYESSYVPKLKOSLSKTLHFFPELSCNLIYPSSPEKMPERPKLSGOSSVSFTTAES
SKDPEDLVGNRPESPVRLYNFVLPPIVEESDRKLFOVPAVQVTLFFGRGVGIGIAT
HHYSDAPSFLAFIPMASSMSKHIENEDEBFRSLPVFORSVYKYPTREDSIVRRNA
LKFPLQSREPSLPTDRIRTTPVFTQSKIKKLKGWIGSRVPSIVHLSSPYAIDAYWWAG
ITKSPTADEDDNEDAFFLIPUDLRPRLDPPVPENTYFGNCLSYALPRMRRRELVGEKG
VFLAAEVIAAEVIAAEIKKRINDKRLLETVEKWSPEIKRALQKSYFSVAGSSKLDLYGAPFGW
GKARKOEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING"
315 c 331 g 411 t
                                                                                                                                                                                                                                                                                                    Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko Sakakibara, Suntory Research Center, Fundamental Research, Plant Blotech; Shimamocto-cho, Wakayamadal, 1-1-1, Mishima-gun, Osaka 1016-8503, Japan (E-mail:Keiko_Sakakibara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262)
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TGACTTTCCACATTCTAAATGCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAATC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 TTCTTTCACCATCGCAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 TCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTCTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 ATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCTCGGGTATATC 484
                     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 TTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 CATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 TGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACGAAATCATCCTCG
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                                                                       1 (sites)
Sakakibara,K.Y., Tanaka,Y., Mizutani,M.F., Fujiwara,H.,
Ashikari,T., Yamaguchi,M. and Kusumi,T.
Molecular and biochemical characterization of a novel
hydroxycinnamoyl_com: anthocyanin 3-0-glucoside-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product."anthocyanin acyltransferase"
/protein_id="BAA93475.1"
/db_xref="G1:7415646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 189.2; DB 12;
48.5%; Pred. No. 1.2e-31;
Live 0; Mismatches 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Perilla frutescens
/db_xref="taxon:48386"
                                                                                                                                                                                                                        2 (bases 1 to 1476)
Sakakibara, K.Y. and Tanaka, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="leaf
<1. .1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=3
                                                                                                                                                                                                     Unpublished (1999)
2 (bases 1 to 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 725; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTATCGGAATCTAATGGAATCCCTTCAAAAAGATTTCTCGGGATTACCGGATCGCCTA 1215
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                                                                            CGAATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTATGGCCTAGAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAAAAGGTCTTAA----CCCAAGTGCCAAACTTGGAGTACATGT--CATCTTTACGG
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                                                                                                                                                   AAGGATCTCCACCGGTTTTTGATAGATTGATTAACA-----TCCCACATTTAGATGA
                                                                                                                                                                                                                                                     AAATAAGTTGAGACATACAAG----GCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTG
                                                                                                                                                                                                                                                                                                       676 CATITIGGAACGAATGCAAGAIGITCTIGAAATGITCTTGTAGAITIGGAAGCAAACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACGGAATCTTGAAAGATGCCGCGAGATGGCATGA---ACCTTTCATGATCCCGGCTAG 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGAATATTAGAAACGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATC 1120
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                    ACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA
                                                                               GGCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGAATTTAAATC
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24-JUN-1998
                                                                                                                                                                                                                                                                                                                          FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKA
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10,
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                                                                                                                                                                                                                                                                              PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                  1 (bases 1 to 1479)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PATENT: JP 1997070290-A 4 18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1479
E12756 1479 bp DNA PAT 24-J
Perilla ocimoides mRNA for acyltransferase,partial cds
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m FT}
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185.8; DB 10;
Pred. No. 6.7e-31;
0; Mismatches 657; I
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism='Perilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone='pSAT208
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/organism="unidentified"
/db_xref="taxon:32644"
1 316 c 331 g 41.
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17-FEB-1995 JP 95P 671
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JP 1997070290-A/4
18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
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ilarity 49.4%;
Conservative 0
                                           E12756.1 GI:3251588 JP 1997070290-A/4.
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E12756.1
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JOURNAL
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ATCTCCCGTTAGGCTCTACAACTTTGTCCCTAAATTGCCGCCCATTGTCGAAGAATCCGA 406
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                       425 TTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC
                                     ACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA
                                                                                                                       AGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGG---ATC
                                                                                                                                             527 GCCTTGGTCTTCAATGAGCAAACACATTGAAAATGAAGATGAAGATGAAGATTTAAATC
                                                                                                                                                                       TCCACCGGTTTTTGATAGAT - - - TGATTAACATCCCACATTTAGATGAAAATAAGTTGAG
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24-JUN-1998

E12754 1622 bp DNA PAT 24-JU Gentlanatriflora mRNA for acyltransferase,complete cds. E12754 E12754 GI:3251586

DEFINITION ACCESSION VERSION

9

RESULT E12754 LOCUS

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TAKAAKI PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                       PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AATCTTTATCGGTCACTCTTCAACATTTTTCCCGTTTGCTAGTAATTTGATTGTATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 CTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1622;
                                                                                                      ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                             /organism='Gentiana triflora'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2e-20;
0; Mismatches 643; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type='petal'
/clone='pGAT106'
35. .1474
/product='acyltransferase'
                                                     1 (bases 1 to 1622)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER
SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 138.2; DB 10;
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
a 345 c 322 g 47
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JP 1997070290-A/2
18-MAR-1997
30-JAN-1996 JP 1996046534
17-FEB-1995 JP 95P 67159
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                                                                                                                                                                                                                                                                                                   (C12N9/10,C12R1:19);
strandedness: Double;
topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                                                               /variety='japcnica'
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JP 1997070290-A/2.
unidentified.
unidentified
unclassified.
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Matches 676; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  1122 CCATCGGAGATGCTATCCATAAGAGGTTACATGACTACGAAGGAATTCTGAGAGGAGTT 1181
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CGGGGGAGGAAGTATACCACTTTTGCTTTACAGGTGACGGTGTTCTCCCAACACGGGTA 521
                                                          TATGCATTGGACGCAATCTTCATCAAGTTCTTGGTGCCAGTTCTTTTCTGCATTTA 581
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                                                                                                                                                                                                                                                                                                  AGAAAAAGGTCTTAACCCAAGTGCCAAACTT--------GGAGTACATGTCAT 807
                                                                                                                                                                                                                                                                                                                           AGAAATTCATTTCGTCAAAAATCGCAACTTAACCGGTAGTAGTAATTATAATCTGTCAA 881
                                                                                                                                                                                                                                                              CTTCTCTACCTATGTACGACAGATCTGTGGTGCAAGATCCATTTCATATTCGTCGAAAAA
                                                                                                                                                                                                                     702 TCTACAATGAAAGAAACTGCTCAAATCTCAGGGCACACCTACTGTTCTAAATCCAGCAA
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                                                                                         ----CGGT
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                                     TATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTT
                                                                                                                                                                                                                                                                                                                                                                                                   868 GAGAAAGAAAGGGCGAAGACG----AGTTAGAACAGTTCATAATCACCATTGATTGTC
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AB026494 1622 bp mRNA PLN 04-APR-2000 Gentiana triflora GAT106 mRNA for acyltransferase homolog, complete ods.

AB026494 LOCUS DEFINITION

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/translation="magnSEDIKVLEKCRVAPPDAVAEFTVPLSFFDMRWLISDAEH
HLHFYRFRHPCPNSKFIISSIKSSLSLVLKHFLPLAGNLIWPVDSSDRMPELRYKKGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGICIGRNLHQVLGDASSFLÄFNKLWVLVDKSNGDSLKFLPLSSLPMYDRSVVQDPFH
INRKIYNERKLLKSGGTPTVLNPAISKDEVRATFILHPIDIMKLKKFISSKNRNLTGS
SNYNLSFFTVYSALIWTCLSKSLDTVVREKVEEDKHAANLCAFINCRORFAPPIPQNY
FGNCIVPCMYGSTHEDLVGNEGLSVAATAIGDAIHKRLHDYEGILGGDMISPRSTSA
APRSTLIYVVGSAQRNVHDFDADFGWGKLEKHESVSTNPSATLLISRSRRFKGALEL
GISLPKNRMDAFATIETNFINSLHVRSPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Tanaka, Suntory Lid., Institute for Fundamental Research;
Wakayama-dai 1-11, Shimamoto, Osaka 618-8503, Japan
(E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana.
                                                                                                                                                                                                                Yonekura-Sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M.,
Yonekura-Sakakibara,K., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular cloning and biochemical characteization of
hydroxycinnmamoyl-CoA.anthocyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AATCITTATGGGTCACICTTCAACATTTTTCCCGTTTGCTAGTAATTTGATTGTATTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 TAGATTCCTCCG------ATAGAATGCCGGAGTTGCGTTACAAGAAAGGGGACT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTCGT 60
                                                                                                                                                                                                                                                                                                                          3-0-glucoside-6-0-hydroxycinnamoyltransferase from Perilla frutescens and diverse plant acyltransferase homologs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 CGTCCCTTTCCCTTGTTCTCAAACACTTTCTTCCGTTAGCCGGGAATTGATTTGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.2%; Score 138.2; DB 12; Length 1622; 48.6%; Pred. No. 2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gentiana triflora"
/db_xref="taxon:55190"
35. .1474
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
2 (bases 1 to 1622)
Tanaka,Y. and Yonekura-Sakakibara,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="acyltransferase
/protein_id="BAA93452.1"
/db_xref="GI:7415597"
                                            acyltransferase homolog.
Gentiana triflora cDNA to mRNA.
Gentiana triflora
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35. .1474
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                       AB026494.1
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                    VERSION
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AUTHORS
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JOURNAL
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101 CTGTTGTGGTACTTTGCAGANTGTGCTTGACTTTAATAATTTGACGGAAATCAC 310 102 CTGTTGTACTATTGCAGANTGGGCATTTGATTGATTTGAT		TON C C C C C C C C C C C C C C C C C C C	REFERENCE 4 40111CC AUTHORS ECKEr, J JOURNAL DEPARTITE JOURNAL DEPARTITE HAMILIC REFERENCE 5 (DAS AUTHORS CHOU, J HOWING, LIU, S., Schwart TITLE DIRECT JOURNAL DEPARTITE HAMILIC HAMILIC HAMILIC AUTHORS CHORY HAMILIC HAMILI	Chiou, Chiou, Chiou, Chiou, Chio, Ch
0 0	762 TITTAAAGTTGAGCCACCTTCATCTTTTTTTTTTTTTTTT	402 AGAGGGATTCTATATATCACGATTTGATTCGCAGCTGCCAGACCGATTGTACCT 421 GTGATTGCTCACCACTTTTTCACTTCAGGTGCCTGCCGGAACCGGTA 421 GTGATTGCTCACCACTTTTTTCACTTTACAGTGACGTTTTTCCGGGCTCGGGTA 481 TATCACTAGGAATCATCATACAGTTGTTTTTCCAACACCGGTA 481 TATCACTAGGAATCATCATCGTGGTGACGCTGTTTTTTTT	868 GAGAAGAAGGACGAAGACGAGTTAGAACAGTTCATAATCACCATTGATTGTC	1264 CATCAGCACAAGATTTGAAATTGGATTGAGTCTACCGAGTATGCAAATGGAGGCGTTTT

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RESULT 8

ACCOCKANTITI 1332

ACCOCKANTIS ACCOCKANTITI 1340

ACCOCKANTIS AC
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us-08-894-356c-5.rge

JOURNAL

FEATURES COMMENT

CDS

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join(11965. 12033,12173. 12303,12448. 12519,12596. 12685, 12756. 12915,12985. 13041)
/note="similar to ATHP1 dbj|BAA37110.1"
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/product="12187.5"
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/db_xxef="61:9286641"
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VARNVOISFRECCDOPREGSSSNSHYRCDNDIWHRCLRCLQQVDYEYKMLKRTKLQDLF
NVSFKLCENLLVLLEKQILQAGGTIPQVDIN"
                                                                                                                                                                                                                                                                                                                        /translation="mrgFSSvSswLwTsvEIGEVFLGSTTWLDAVAVAEDAVDWwVFS
ACLMVNKLDLRWLLRVPVAEGLSEPSPFFSLRFLSPSIRIEGCFAFGKFSDLRFWRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIVPGRIMGALPATISQLKDLRFLAISRNFISGEIPASLGEVRGLRTLDLSYNQLTGT
ISSSTGSLBELSNLILCHNHTGSIPPELSQTITRIDLKRNSTGSISBASLPPSLQY
LSLAWNQLTGSVYTHLIRLNQLNYLDISLNRFTGTIPARVFAPPITHLOLQNRFFEGI
IQPANQVTISTVDLSYNRFSGGISPLLSSVENLYLNSNRFTGEVPASFVERLLSANIO
                                                                                                                                                                                                                                                                                                                                                                                                  AWKCVVVLRGWGLDQIGWRSVGNWVFSVRFVAGPASSLVRDLRQDSYTSANDLVPVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRFTKLVWCLMFLLRFGFFTEAILDPVDFLALQAIRKSLDDLPG
SKFFESWDFTSDPCGFAGYYCNGDKVISLNLGDPRAGSPGLSGRIDPAIGKLSALTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLYLQHNFLTGIQISPAAEIPVSSSLCLQYNCMVPPLQTPCPLKAGPQKTRPTTQCTE
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19064..19139,19214..19410,19497..15595,19668..19752,
19865..20103.20179..20255,20345..20649,20798..20902,
21088..21216,21356..21437,21513..21608,21780..21849,
21929..22025,22408..22552,22586..22659,22810..22888,
23041..23101,23206..23315,23411..23555))
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PQNIVCGHTLTAVFVNNSHQLILFGGSTTAVANHNSSLPEISLDGVTNSVHSFDVLTR
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GGETPSPRYGHVMDIAAQRWLVIFSGNNGNEILDDTWALDTRGPFSWDRLNPSGNOPS
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VFGGSKLHVIGGILNRARLIDGEAVVADTNQPETSASGANRQNQYQLMRRCHHAAASF
SVAIVESTFMRAYSRVYGPIKDLLSAENPAKYRDCTLTEFSTIFSSKTLDAPKLHHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16495. .17682

Anotes—"similar to protein kinase pirl|A57676; similar to

ESTS gbla1993651.1, dbj|AV538995.1, dbj|AV522524.1, and

dbj|AV538995.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 37271 AACATCGAGACCTGTCACATCTCTCCCCCAAAGGGCACCGTTGCATCCACCACTTT 37330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST emb|230724.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 101176;
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Pred. No. 3.5e-15;
0; Mismatches 698; Indels
                                                                                                       similar to
                                                                                                                                                                         /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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/db_xref="G1:9280640"
                                                                                                       /note="unknown protein;
/codon_start=1
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Matches 613; C
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ITILLQDNIGGLQVIHDQCWVDVSPYPSALVTNIGDLLGISKHTDFSF
ITILLQDNIGGLQVIHDQCWVDVSPYPSALVTNIGDLLGISKNFTSAEHRYTANGS
SEPRISMPCFVSTFMKPNPRIYGPIRELLSGNPAKKRDLISTBSPRITATE
IPALFRATPATLALSSPPRHLTIPTVDLKGASVVERIGEAASKWGLFHLVNHGIP
VEVLEMNIQGIRGFHEQEPEAKKRFYSRDHTRDVLKFSNHDLQNSEAASWRCTLGCYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="April"
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LSPQFFTSSPSLSPSSSSGGSSFMARYAMESSKQLANGIINLGDMGYXTLSKYCQDML
PDGSTSPASPNAIWKVGGVSGSDAENAGMVAVKDLVSGALVSQFKAHTSPISALCFDP
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KVEPIQWWDVCRRSDWLETEERLPKSTTEKQYDLETVSNHLTSHEDACLSLDMNSHFS
EDKYLKSCSERPPERSHCYLSNFEVKYTSGMLEVWONSKISHTWBDSPRDSSSTGGEF
EIEKVPAHELEIKQKKLLPVPDHFHSTRATLEDRFSMCYHSTAGGSHQVNGKICQDI
INCHSKPGSLESAESSEEGSTRQMENHDSDHMSNSIKSSLPLYPTVNGIYKETEKNN
ANGWMEKPVTAKLSTLKETRITNGFTTPPILLTDSVNEQMLSTGKPPMGFGFALHEEHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGTLLVTASVCGNNINVFQIMPSRSHNAPGDLSYEWESSHVHLFKLHRGITSAIVQDI
CFSQQSQWVAIISSKGTCHIFVLNSSGSDAAFQPCEGEEPTRLPASSLPWWFTQSLSS
NQQSLSPPTAVALSVVSRIKYSSFGWLNTVSNATTAATGKVFVPSGAVAAVFHKSVTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MASCIQELHFTHLHIPVTINQQFLVHPSSPTPANQSPHHSLYLS
NLDDIIGARVFTPSVYFYPSTNNRESFVLKRLQDALSEVLVPYYPYPLFSGRLREVENGKL
EVFFGEEQGVLMVSANSSMDLADLGDLTVPNPAWLPLIFRNPGEEAYKILEMPLLIAQ
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PPMVKYPHHEYLPIEERSNLINSLWDTKPLQKCYRISKEFQCRVKSIAQGEDPTLVCS
TFDAMAAHIWRSWVKALDVKPLDYNLRLTFSVNVRTRLETLKLRKGFYGNVVCLACAM
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VGQHYPPCPQPDLTIGINKHTDISFLTVLLQDNVGGLQVFHEQYWIDVTPVPGALVIN
IGDFLQVKKIMLLLRSCFISCMIWGLILLFYCVQLITNDKFISAEHRVIANGSSEPRT
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FEMY ETADFGWGKPVYAGPI DLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
                                                                                                                                                                                                                                                                                                                                                  join(736. 1038,1276. 1713,1874. 2119,2205. 3032, 3117. 3274,3483. 3610,3725. 4134,4313. 4435)
//note="unknown protein: similar to ESTS dbj|AV529515.1, dbj|AV529266.1, dbj|AV54950.1, dbj|AV523761.1, dbj|AV523761.1, and dbj|AV540743.1"
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//note="unknown protein; similar to ESTs gb|T04168.1,9b|T21964.1, and gb|AW004462.1"
//codon_start=1
                             Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On Jul 15, 2000 this sequence version replaced gi:2618677. Location/Qualifiers
Submitted (19-JUL-2000) Arabidopsis thallana Genome Center
                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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/note="hypothetical protein"
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                                                                                                                                                                                                                                                                                   /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                        /clone="F21B7
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AAGTATTGGATGTCATTGACCAAATCCAGGGGCAAAGATCCGGCCACGGTTCTTCTACCC 37861
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                                                                                                                                                                                                                                                                            37568 GTAGCAGAGTCTACTGAAACCGACTTCGACCAACTGAAGTCTGATTCCCCTAAAGATATC 37627
                                                                                                                                                                                                                                                                                                                                                                                                                                           37688 CA-----GATGCGACCAATAATGGCAATGCAAGTCACCATCTTCCCTGGAGCTGGAATC 37741
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123 TATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAA
                                     TTCTCTTACCAAAACTCAACTGAATCTTTCCTCCAAGACTTTGTACCCAACCTCAAACAT
                                                                                                  37742 TGTATAGGCAACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTCATTTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37982 AACATGGTCAGAGCCACTTTACATTGAGCCGGAAGCAGATAGACAATCTCAAGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTTAACCCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38042 GTTACAGAGCAGTCTGAGAATCAATCTCCTGTTTCTACCTTCGTGGTGACTCTAGCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCT
                                                                                                                                                        AACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAAACACGTTGAAGGTGATTCT
                                                                                                                                                                                                37511 GGTCCCGACCCTCCATATTTACACTACAACGCTG---GCGAAGACTCTCTTGTTTTCACC
                                                                                                                                                                                                                                        GTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCT
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                                                                                                                                                                                                                                                                                                                        CGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGT
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Eukaryota, Viridipulae, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 119914)

1 (bases 1 to 119914)

1 Federspiel, N. A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Hulzar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, W., Yu, G., Ekker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA Sequencing and Technology Center, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
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dence with similarity to proteins in the databases are described
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'
The software programs used to predict genes include: Grail
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Direct Submission
                                                                                                                                                   38522 ATCGCATTCTCAGAGTCCAGAGACGGCAGCAATGGAGTTGAGATTGGAATAGCACTAGAG 38581
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Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P. Gonzalez, A., Kremehetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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Bases 19262 of clone F21M11 overlap with bases 6899877825 of
'TAMU' BAC clone F20D22 (ACO0241) and bases 119525-119914 of
F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic sequence
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ATTTCTATAAATGCAAGCAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana chromosome I BAC F21M11
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                     AAGAAGAAATGGATGTGTTT 38602
                                                                                                                                                                                                                    1302 AGTATGCAAATGGAGGCGTTT 1322
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3 (bases 1 to 119914)
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Arabidopsis thaliana
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SOURCE
ORGANISM
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AUTHORS
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join(20752. .2094,21362. .21497,21596. .21740,21825. .21994,
22102. .22178,22542. .22758,22920. .23064,23343. .23442,
23599. .23693,24021. .24072,24227. .24298,24441. .24647)
/gene="F21M11.5"
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                                            DSLANPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGGGVLNPVENLTOWKSAR
KRFRYKQFQSQKENSNFIADOBEKRDSSSFGTPDQIDDITLSVWFKCR EPKKLRNQE
LAVDASLSTWLSTESEGSECNSASMYTLTPEKLKSTSCYSKPLRIHDDRPVLCALTL
EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="Aad10669.1"
/db_xref="G1:4204288"
/db_xref="G1:4204288"
/translat-ion="MGSSPBRRARAQVPSMILIFLEIICTVHVYTNRRKLNRDVLSANLINTRNRENLERPSVI5.1785.1NAAVSVHLPOLQIPNCCNYKNDALNNSNSPKHGESEDSEMTDKDVSKRSGGTDSSSRDGSPLPTSEESDPRPKHQDWTEKQLSDHLLLYE
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TLLRIMESIRSDDPTDYVKAQNHQWYYFSFWYIYSPYLCLERNNLRCWYIFCWQLPK
SHTEQDSKRKRDITASDAAMHLKVPKPRENNLAMGKSADIDCNGKCSANSDDQLSEKIS
KALEQDTSKRYTICGCCQSARYSEATGEMLHYSRGRPWDGDDI FRSWYIHYHSACIEWA
PQYYYEGDTYKNLKAELARGMKIKCTKCSLKGAALGCFVKSCRRSYHVPCAREISRCR
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GDFYKGYKEDLQNLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVXNIDPPHGCAL
GEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
20752. 24647
/gene="F21M11.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WDYEDFILLCPAHSSVKFPNEKSGHRVSRAEPLPKINPAELCSLEQTPAFTKELVLCG
SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKW
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RPPPKNVGCIYGAHLKTBVGYYRABGKRYPDMNIITDIIYETEGSLVSRSGTVVDG
NAGPITGDETVPYBLSLWCKNWLGRKVNITMAPQIIJGKIKQDPEHDGSDVHVELNVD
HEHGSDIIANMTKAPRVKYIIFYEDSESIPGKRTAVWELDKSGY"
        TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEEYYSDVGFSE
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31782. .32033))
                                                                                                                                                                                                                                                                                                                                              complement(join(16835. 17185,17274. 17392,17491. 17656
17795. 17885,17982. 18079,18175. 18361,18504. 18604,
18705. 19049,19134. 19349,19439. 19791,19862. 19967,
20188. 20238)
/gene="F21M11.4"
/note="Hypothetical protein"
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gb|H76794 and 203124XP, gb|AA605510"
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Pred. No. 1.9e-09;
); Mismatches 718;
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                                                                                                                                                                                                                 REDKSVNWHSTPFEARLEKALNNIDK"
complement(16835. .20238)
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/db_xref="GI:4204289"
                                                                                                                                                                                                                                                                                                     /gene="F21M11.4"
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/gene="F21M11.6"
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28007. .28465
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EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
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ECETSGDGMSKAISNNKDITAGEENVETPWNBIETNEKYPSRFXMPHSFYFQDAPVIFS
LSSFSDBGSCSTSCIEDCLASMSONCAIGVDNGFAYTLDGLLKEFFLEARISEARDO
RKQVLRFCEECPLERAKKVEILEMSCKGHLKRCAIKECWFKGGCTKRCNRVVQRSMHN
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KGRYDLAKGYCESWRINVEVHNIRKEDVPQECVSHIKDYWTSSQYKDDVSRYVDEVI
LHFGSWCCSKSKCDGMDANIPIDDTLLSTIPYHKNEFFEGEKLNSTKFEDNIQKK
APAVPHMKKLYHDIRERGIKIFLISSRKEYLRSATVDNLIQAGYYGWSNLMLRGLEDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Proteins in this region are annotated in the F2lMll entry, AC002411."
1. .9262
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DAYKVLLDAIFDEADAQSTEKNKKEEEKKKREEEKKSRSVATSRGRRKAPEPLVQDEE
DDMDEDEFPLKRRLRSRRGRASSSSSSSSYNNEDLKTQPEEEDEDDGVTELPPLKRY
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WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
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complement(join(14004. .14312,14565. .14641,14787. .15831,
15906. .16006,16327. .16362))
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16327. .16362))
/gene="F21M11.3"
(Informatics Group, Oak Ridge National Laboratory, http://compblo.cnnl.gov/section/index.html, GENSGAN (Chris Burge, http://gnomblo.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="overlap with bases 68998-78259 of 'IGF' BAC clone F21M11."
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join(13033. .13488,13717. .13926,14139. .14514)

/gene="F21M11.2"

/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9893,10003. 10256,10344. 10410,10501. 10551,10685. 10781,10885. 10913)
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/gene="F21M11.2"
/note="Similar to acid phosphatase; Location of
1100277, gb/142036, and 110C2XP, gb/A1100245"
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    119914
    /organism="Arabidopsis thallana"
    /cultivar="Columbia"

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complement(14004. .16362)
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/db_xref="GI:4204284"
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/db_xref="G1:4204285"
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/db_xref="G1:4204286"
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/chromosome="I"
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/gene="F21M11.1"
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GTAGCAGAGTCTACTGAAACCGACTTCGACCAACTGAAGTCTGATTCCCCTAAAGATATC 46309
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                                                                                                   123 TATGACTITCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAA
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AACATTCTCGAACATGCCCGAATATCGGCCCCCCTCGGGCACCATCGGCCATCGCTCGTTA
                                                 TCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTC
                                                                                                                                                     TCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCT
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YEPDONDGYSFRAMAIENRSILENEKHENSTFTLLHYTDHAGHIMMEDAKKRAV
YEPDONDGYSFRAMSSECHAGFHILSGNGIRGAVEFHPLVPQLSJTDDKARVIA
TILFPNGGFSIGVSSHHAILDGKTSTLFLKSWAYLCKQLQLCHHPCLSPELTPLLDRT
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ANABAIRANDRKVSEILEILKGAMIFSVAGSTQFDVYGSDFGWGRPKKVEIVSIDRTQ
AISLAFRRDGGGGRVENGTGGGWAYFESVFADGLKNDLV*
344 C
354 9 46 E
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Fruit flavour related genes and use thereof
Patent: WO 0032789-A 40 08-JUN-2000;

AHARONI ASAPH (IL); VENDEVEN HARRIE ADRIANUS (NL); LUECKER JOOST (NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN JOHANNES VAN (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1648)
Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and Van
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47264 ATAGCACTAGAGAAGAAGAAAATGGATGTGTTTGACTCCAATTCTACAACAGGGGATCAAG 47323
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                                                                                                                                                                 47204 ACAGGTGGTTCTATCGCATTCTCAGAGTCCAGAGACGGCAGCAATGGAGTTGAGATTGGA
                                                                                                                                                                                                                                                                                                              TTGAGTCTACCGAGTATGCANATGGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAG
                                                            GAACCTTTCATGATCCCGGCTAGGAAG---ATTGGTGTTGCTGGTACACCTAAGCTCAAC
                                                                                                                                            1170 TTGTACGACTTTGATTTTGGGTGGGGAAGCGCATAAAGTATGAGACTGTTTCAATAGAC
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/db_xref='taxon:2708"
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/codon_start=1
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Sequence 40 from Patent
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For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi.bin/agd_graph.cgire_MKTD.

For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi.bin/agd_graph.cgire_MKTD.

Foreswith similarity to proteins in the databases are described in
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail

Informatics Group, Oak Ridge Mational Laboratory,

http://compbio.ornl.gov/Grail-1.3/),
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Kakaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicacae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                  1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1139 GATIGGIGITGCIGGIACACCIAAGCICAACTIGIACGACTITGATITIGGGIGGGGAA 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1302 TTTTCTGTGGCTGGCTCGACCCAATTGATGTTTACGGGTCGGATTTCGGGTGGGGGG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCATAAAGTATGAGACTGTTTCAATAGACTATAATACGTCGATTTCTATAAATGCAAG 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTATGCAAATGGAGGC 1318
                                                                                                                                                                                                                                                                                                                                                                            GGTTGCTTTTGTTGCAGAGATGTTAAGTGATATGGTCAAAGGGATCGATGCGGATGCCAT 1241
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1002 CAAAGCCAAAACTGAAGCTGAAGCTGCAGCAAATAATGATGAAATTAAAAATATTATTGT 1061
                                                                                                                         1062 GGGATTCACTGCGGATTATAGGAGCCGTTTGGATCCTCCAATTCCACTTAATTATTTGG 1121
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MXF12.
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Submitted (18-MG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0912, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1122 TAACTGCAATGGGAGACATTGTGAGACTGCAAAAGCAAGTGATTTCGTTCAAGAAAATGG
                                                                                                                                                                                                                                                                                                               1022 GTATGCACTTGGTGCTAAAGTAATTGGAGA---GTCTATATGCAAAATGATATAATAA
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                                                            902 CATAATCACCATTGATTGTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTTTGG
                                                                                                                                                                                      962 TAACTGTGGTGCACCATGTGTCCCGACCTTAAAAAATGTCGTTTTGACTACGGAAAATGG
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SNYRRGTVDQIIDSDLSADITSTSLEKFCEIAVRCVQDRGMERPPMNDVVWALEFALQ
LHETAKKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
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VSGRNWTARDKILSSNLVNASFTAGASYGESOVSQIPVMTARIFRSEPETYSFPVTPG
VSGRNWTARYPTRYGODNAVKSFSVKVNGFTLLNNSADLTVKASKPOTEIIKEFI
IPVYQTLNLTFTPSGLOSLAFVNGIEIVSIPNRFYSKGGFDDVIINVGSSVDFHIENST
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/protein_id="BAB10825.1"
/db_xref="G1077546"
/translation="MINLEKEAKEKQILIRDGKRKIVHHVNTTLLVKIYEASAIDDRH
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RNWTVESRQILSSNLVNASFTSEASYQKAGVSRIPYMKARIFRSEFTYSFPVTPGSIF
LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
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SVHRLNVGGQIVNEVDDSGMFRRMLSDDSFGNSGSIVNVPGVKINYTEKTPAYVAPYD
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ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRMYGGISHKSDVY
                                                                                                                                                                                                                                                                                              (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K15E6 and the 3' clone is K3K3.

Location/Qualifiers
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GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
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SGVEILKLNDSDGNLARPNPELLVSTDSTPDDSNVTPPIKGKPHVLVIILIVVGSVIG
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KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
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NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University
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/codon_start=1
/evidence=not_experimental
/product_receptor_protein kinase-like protein"
/protein_id="BAB10826.1"
/db_xref="GI:10177547"
                                                    Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE
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DTLIDLLIGERIT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTAACTGTGGTGCACCATGTGTC--CCGACCTTAAAAAATGTCGTTTTGACTACGGAA 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26478 GTTGCATTGAAGATTCCAGAGATTTTGGAAGGGTTTACGACTCTTTCACCAGGAACACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72.6; DB 12;
Pred. No. 5.1e-06;
0; Mismatches 239;
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Sequence 22 from Patent WO0111061.
AXO83744
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synthetic construct
artificial sequence.
1 (bases 1 to 1141)
Kunst, L. and Clemens, S.
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Matches 228; Conservative
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10in (25348). . 26559, 26401. . 26756)
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FGTVYGGNLSNGRKVAVKVLKDLKGSABDFINEVASNGOTSHVNIVSLLGFCFBGSKR
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GVGFWFTSSWKLTLLALVVVPVISVAVKQFGRYLRELSHTTQAAAAVAASIAEBSFGA
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TITTYGSMYTVGALTSFILZSVSYSSLSSLTTAMKAAGASRRVBOTLDRYSSMS
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                                                                                                                                                                                                                              WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
RLYFYPTSYKSGFDAVNSFVSVTVNDFTLLQNPSADLTVKASIPESKSLIKEFIVPVY
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QNILLDGNLCPKVSDFGLAKLCEKRESVLSLMDTRGTIGYIAPEVFSRMYGRVSHKSD
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SSSSVSSSPKELRLSTFV1VYSYALTCL1KARGGDPSRPVGYGFAVDCRSLMVPPVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(16412. .16498,16859. .16924,17003. .17038,17085. .17337. .17461,17541. .17640,17803. .17974,18073. .18191,18285. .18395,18488. .18632,18712. .18844,18934. .19009,19322. .19297,19385. .19492,19591. .19698,19873. .20070,7004e."gene_id:MXF12.6"
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complement(joln(1,0804, 30874, 30947, .31289))
/note="contains similarity to Ac-like transposase
                                                                                                            /product="receptôr protein kinase-like protein"
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                                                                                   /evidence-not_experimental
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                                                                                                                                                                                                                     ATCGCTCGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACC 1111
                                                                                                                                                                                                                                      112 ATCTTTCTTCTAGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCA 171
                                                                                                                                                                                                                                                                                                                                                    GGCTAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGA 231
                                                                                                                                                                                                                                                                                                                                                                                   412 AWYWKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRAWDHKTCTHNNTT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
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                                                                                                                                                                                        Gaps
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/organism="synthetic cc/db_xref="taxon:32630"
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1132 CDGARYW 1138
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Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequencia conservation of the co
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                              CNSO6V7I 805 bp DNA STS 11-JAN-2001
T7 end of clone AXOAA017D07 of library AXOAA from strain CBS 7064
of Pichia farinosa, sequence tagged site.
                                                                                                                                                                                                                                                      Pichia farinosa.
Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 805).
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrans, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuvedise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1) FEBS Lett. 487 (1), 3-12 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                               de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiguenave, F. and Potier, S. Genomic Exploration of the Hemiascomycetous Yeasts: 15. Pichia
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/strain="CBS 7064"
/db_xref="taxcn:4920"
/clone="AX0AA017D07"
/clone_lib="AX0AA"
/note="end : T7"
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38.8%; Pred. No. 0.
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FEBS Lett. 487 (1), 87-90 (2000)
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Direct Submission
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1 (bases 1 to 321003)
8 Moman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFMAL4P3 321003 bp DNA HTG 19-AUG-1999 Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                          1411 ATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAAC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTCTATG 126
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                                                             |: | : | : | : | : | | 291 AWITITGKITATKKATWGAGGWAKWWITITGKKACTITITITTTTTTTTTGGWKAWTKT 232
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Dorner,F., Schafflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                  h 3.6%; Score 53.6; DB Similarity 1.9%; Pred. No. 0.083; 5; Conservative 171; Mismatches
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Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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                                                                                  On Aug 24, 1999 this sequence version replaced g1:5731899.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1235 TACGTCGATTTCTATAAATGCAAGCAAAACATCAGCACAAGATCTTGAAATTGGATTGAG 1294
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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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/product= Aromatic acyl transferase.
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Best Local Similarity 99.7%; Pred. No. 0;
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Fukui Y,
ura K;
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Ashikari T, Fujiwara H, Fuk
Nakao M, Tanaka Y, Yonekura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aromatic acyl transferase; transformation; anthocyanin pigment; plants; ecylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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                                                      CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA
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                                   ---TATGTGATTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six aspecific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCA---TCGGCCATCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
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                                                                                                                                                                                                                                                                                                                                                           Kusumi T, Mizutani
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                                                                                                      /product- Aromatic acyl transferase
              pGAT4).
              triflora var. japonica (Clone
                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 53-57; 94pp; Japanese
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Nakao M, Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
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P-PSDB; AAW04722.
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29-JUN-1995;
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245 CACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAAACACGTTGAAGGTGATTCTGT

TTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC 484

tagaaaactcttccaagttttcgccgtgcaggtgactctttcccaggccgaggcgtcgg ACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA tattggaatagcaacgcatcacaccgttagcgacgccccgtcgtttctcgcgtttataac AGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGAAAGG----ATC ggcttggtcttcaatgagcaaacacattgaaaatgaagatgaagatgaagatttaaatc TCCACCGGTTTTTGATAGAT - - - TGATTAACATCCCACATTTAGATGAAAATAAGTTGAG ACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGATAAAGT 647 gagaaacgcgctaaaatttcctttgcaatctcgtcatccctcattaccgacggaccgcat

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                                                                                                                                                                                                                                                                                                                                                                                                   plants
tone,
                                                                                   anthocyanin pigment;
on; colour change;
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                                                                                 Aromatic acyl transferase; transformation; anthocyanin
plants; acylation; colour; tone; colouration; colour cl
Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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                                                                                                                                                                               /*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                       Fukui Y, Kusumi T,
                                                                                                                Scenecio cruentus; Lavandula angustifolia; ds
                                                             Aromatic acyl transferase coding sequence
  BP.
1479
                                                                                                                                                      Location/Qualifiers 3..1343
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 65-69; 94pp; Japanese
                                                                                                                                     Perilla ocimoides (Clone pSAT208).
  to mRNA;
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                                                                                                                                                                                                                                                                        96JP-0046534.
95JP-0067159.
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  CDNA
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P-PSDB; AAW04725.
 AAT37311 standard;
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29-JUN-1995;
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togaaccacgttcgttttcacccaatccaaaattaagaaattgaagggttggattcagtc 766

TCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTCTTAAAC

CCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTATATATGGAG

179 167 839 827 899

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tttettgatteeggtegatetaaggeeacgattagateegeeggtteetgaaaattaett 940

881

GTTCATAATCACCATTGATTGTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTT

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1181 gaaggcgagaaagcaagaaatattgtcgattgatggggagaaatatgcaatgacrctttg 1240
959 TGGTAACTGTGGTGCACCATGTGTCCCGACCTTAAAAATGTCGTTTTGACTACGGAAAA 1018
                                                                                  1019 TGGGTATGCACTTGGTGCTAAAGTAATTGGAGAGTCTATATGCAAAATGATATAATAA 1078
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                                         941 cgggaactgcttatcgtacgcgctgccgagaatgcggcggcgagagctggtgggagaa
                                                                                                                         GGACGGAATCTTGAAAGATGCCGCGAGATGGCATGA---ACCTTTCATGATCCCGGCTAG
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                                                                                                                                                                                    CATTCTCGAACATGCCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTTATC
                                                                                                                                             33;
                                                                                                      Length 1479
                                                                                                                       Pred. No. 1.6e-34;
0; Mismatches 657; Indels
                                                                                                    DB 17;
                                                                                                    12.3%; Score 185.8;
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Query Match

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313. NOTE: This sequence is supposed to cross reference with the protein described in AAM04727. Anowever there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727, that the indexer decided
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tone,
                                                                                                                                                                                                                            Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
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1313 GGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAGGTCAA 1355
                    /*tag= a
/product= Aromatic acyl transferase.
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                                                                                                                                                                                                 Aromatic acyl transferase coding sequence.
                                                                                                         ВР
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                                                                                                      AAT37313 standard; cDNA to mRNA; 1518
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11.0%; Score 166.6; DB 17; Length 1518; 48.0%; Pred. No. 5.2e-30;

0; Mismatches 744; Indels

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Matches 726;

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Query Match Best Local Similarity

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                                                                                                                                                                                              CTA---GGAAGATTGGTGTTGCTGGTACACCTAAGCTCAACTTGTACGACTTTGATTTTG 1188
                                          GGTGGGGGAAGCGCATAAAGTATGAGACTGTTTCAATAGACTATAATACGT---CGATTT 1245
                                                                            CTATAAATGCAAGCAAAACATCAGCACAAGATCTTGAAATTGGATTGAGTCTACCGAGTA 1305
                                                                                                                                                                  a------atcatgtattatgaagttggatgaaatcctctgtttcatctctattgtt 1412
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                       1123 aaaactgttatttctcggtggcgggatcgagcaggcttgatctttacggcgcggattttg
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                                                                                                                                                                                  1426 TCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGCAACGATATAAAATGAAAA
                                                                                                              TGCAAATGGAGGCGTTTTCTAGCATCTTTGATGAAGGATTAGAGAGTCAAGTTTCATTGT
                                                                                                                                                 AGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGT
                                                                                                                                                                                                                                                                                                                                                     Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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                                                                                                                                                                                                                                                                                                                                                                                 Scenecio cruentus; Lavandula angustifolia; ds.
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/transl_except= ATC encodes
1322..1324
                                                                                                                                                                                                                                                                                                                                     Aromatic acyl transferase coding sequence.
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/*tag= a
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95JP-0067159.
95JP-0196915.
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|1473 aaaaatgaaaaaa 1485
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17-FEB-1995;
29-JUN-1995;
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                                                                                                                                                                                                                                                                           Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six aspecific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                        plants
tone,
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Pred. No. 6e-23;
0; Mismatches 644; Indels 72;
                                                                    coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1622 BP; 478 A; 354 C; 313 G; 477 T; 0 other;
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Matches 675; Conservative
P-PSDB; AAW04723
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                                                                                                 GAGAAAGAAAGGGCGAAGACG----AGTTAGAACAGTTCATAATCACCATTGATTGTC
                                                                                                                                            TCCCGACCTTAAAAAATGTCGTTTTGACTACGGAAAATGGGTATGCACTTGGTGCTAAAG
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                                                             CTTTTACGGTAACTTGTGGTTATATGGAGTTGCATAGCGAAATCACTCGTAAAAATAG
                                                                               ctttcacggtgacatctgcactgatctggacatgcttgtcgaaatcattagacaccgtcg
                                                                                                                                   GATCTCGTCTTGATCCACCAATTCCCACAGCCTACTTTGGTAACTGTGGTGCACGTGTG
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                                                                                                                                                                                                                                                                                GTACACCTAAGCTCAACTTGTACGACTTT-----GATTTTGGGTGGGGGAAGCGCATAA
                                                                                                                                                                                                                                                                                                                    AGTATGAGACTGTTTCAATAGA---CTATAATACGTCGATTTCTATAAATGCAAGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                          AGAAAAAGGTCTTAACCCAAGTGCCAAACTT-
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETW) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other
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Matches 7; Conservative 474; Mismatches
                                                                                                                                                                              Example 6; Page 127; 159pp; English
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WPI; 2001-159728/16
                                                                                    hybridization as:
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
    AAAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAAATAAG 653
                                                                                                                                                                                                                                                                             TTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT 713
                                                                                                                                                                                                                                                                                                                                            AAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAAAGAAAAAGGTC 773
                                                                                                                                                                                                                                                                                                                                                                       TTAACCCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTATATA 833
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                                                                                           TCGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTC
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AAF58257/c
ID AAF58257 standard; DNA; 936
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17-MAR-2000; 2000US-0190259.
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                            mismatch; genotyping;
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Best Local Similarity 0.9%; Pred. No. 1.7e-19;
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17-MAR-2000; 2000US-0190259
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                                                                                                                                           different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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1larity 0.9%; Pred. No. 1.7e-19;
Conservative 474; Mismatches 283;
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group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                group, useful as labels in allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
                                                                                               TTAACCCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTATATA 833
                                                                                                                              AAAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAAATAAG
                                                        TTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT
                                                                            for genotyping,
                                                                                                                                                       иментиниминимимимимимимимимимимимимимими 25
                                                                                                                                                                                                                                                                                                   Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 0.9%; Pred. No. 1.7e-
Matches 7; Conservative 474; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and single-nucleotide polymorphisms, e.g. monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                         BP
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                                                                                                                                                                                                                        AAF58262 standard; DNA; 936
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                            TCGGGTATATCACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTC 533
                                                                                                                                                                                                                                                                                                           TTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT 713
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                                    CTAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATT
                                                                                    GTATTTCCTAACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAACACGTTGAA
                                                                                                                                    294 GGTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGA
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gene expression; ss.
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Length 936; Indels

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774 TTAACCCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTATATA 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                     AAF58252 standard; DNA;
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                                                                                                                                                                                                                            The present invention relates to a composition comprising two nucleic acids each conteining an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAAGGTC 773
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                                                                                                                                                                                                                                                                                          single-nucleotide polymorphisms, e.g. for genotyping
                                                                                                                                                                                                                                                                                                                                       Seguence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                                                                                                 Example 6; Page 127; 159pp; English
                                            (CLIN-) CLINICAL MICRO SENSORS INC
26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                          monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 GGCTAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGA 231
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hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                              Electron-transfer group, ETM; mismatch; genotyping;
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                                                           Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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Example 6; Page 127; 159pp; English
                                                                                              Query Match
Best Local Similarity
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                                              471
GAAATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAA 411
                              CGAAAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAATA 651
                                                                                                                                                            652 AGTTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTG 711
                                                                                                                                                                                                            ATAAAGTTCGGTCAACGTTTGTGTTGACCCGAACTAATATCAATCTACTAAAGAAAAGG 771
                                                                                                                                                                                                                           TCTTAACCCAAGTGCCAAACTTGGAGTACATGTCATCTTTTACGGTAACTTGTGGTTATA 831
                                                              TCAACTTTTTGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTAA
                                                                                                                                                                                            TCAAATTATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTCCGG
                                                                                                                             GCTCGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGT
                                                                                                                                                                                                                                                                                                                                                                                             Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259
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The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                             Score 118.2; DB 22;
Pred. No. 1.1e-18;
59; Mismatches 282;
                                                                                                                                                                                                                      Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGGAGTTGCATAGCGAAATCACTCGTAAAAATAGG 868
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group, useful as labels in allowing repeat analyses on
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                   532 TCAACTTTTGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAA 591
                                                                                                                                                        AGTTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other
                                                                                                                                                                                                                                                                                                                                                                                         TATGGAGTTGCATAGCGAAATCACTCGTAAAAATAGG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping, a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 ATCTTTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCA 171
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59; Mismatches 282;
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                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
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17-MAR-2000; 2000US-0190259
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AAF58257;
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Best Local Similarity 0.8%; Pred. No. 1.1e-18;
Matches 6; Conservative 469; Mismatches 282; Indels
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Sequence 10, Appl
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/RE_COMB.seq:*
/cgn2_6/ptodata/2/ina/RE_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-821-994-64
US-08-924-747-25
US-09-247-373B-25
US-09-296-715-25
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                                                                                                                                  November 5, 2001, 18:04:45
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - nucleic search, using sw model
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length: 2000000000
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US-08-361-441B-14
US-08-379-482A-2
US-08-446-855A-1
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US-08-545-196B-12
US-08-545-196B-12
US-08-207-904-16
US-08-171-385-27
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ALIGNMENTS

SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECCMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria 30472/114 IMMU FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 III PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: (703)836-9300 LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single (703)683-4109

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Query Match
                                     Matches
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                                                                                                                                                                             67 ITACTITCTICGACATIACTIGGCIACTCTICCCTCCGGTCCACCATCTTTTCTTATG 126
                                                                                                                                                                                                                             ACTITCCACATICTAAATCCCATTICATGGACACIATIGTICCCAGGCTAAAACAATCTI 186
                                                                                                                                                                                                                                                                                                       187 TATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTAACA 246
                                       Gaps
                                                                           7 TTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTCGTTATCTC 66
3.6%; Score 53.6; DB 1; Length 7218; llarity 1.9%; Pred. No. 0.00017; Conservative 171; Mismatches 90; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Kapil
TITLE OF INVENTION: Parasitic Nematode Tranglutaminase
TITLE OF INVENTION: Proteins, Nucleic Acid Molecules and
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,420
FILING DATE: December 3, 1996
CLIASSIRICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                      1417 YYYYYYYYYYYYYYYYYGTACCAAA 1442
                                                                                                                                                                                                                                                                                                                                                                                  247 CTGATGGTTCGGGTTTTAATAAAAA 272
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
18-08-781-420-10
Sequence 10, Application US/08781420
Patent No. 6248872
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MOLECULE TYPE:
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; LOCATION:
US-08-781-420-10
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Score 47; DB 4; Length 1472;
Pred. No. 0.0048;
0; Mismatches 70; Indels
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Proteins, Nucleic Acid Molecules and
Uses Thereof
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,420
FILING DATE: December 3, 1996
                                                                                                                                                                                                                                                    Score 47; DB 4;
Pred. No. 0.0048;
0; Mismatches 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heeka Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08781420
Patent No. 6248872
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Mehta, Rapil
ITLE OF INVENTION: Parasitic Nematode
ITLE OF INVENTION: Proteins, Nucleic
ITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: December 3, 1990
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37, 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: HW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/A93-7272
TELEFAX: 970/A84-9505
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
    3.1%;
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Best Local Similarity 56.08
Matches 89; Conservative
                                         89; Conservative
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CORRESPONDENCE ADDRESS:
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                       Best Local Similarity
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1362 TIGTAGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCA 1421
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;Patent No. 5340934
; APPLICANT: TERMINE, JOHN D.:YOUNG, MARIAN F.;FISHER, LARRY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Indels
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: Microsoft Word for Apple, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                              GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M
APPLICANT: Girl, Judith G
TITLE OF INVENTION: Interleukin-15 Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44.6; DB Pred. No. 0.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/300,903A
FILING DATE: 06-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/236,919
FILING DATE: 06-MAY-1394
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1482 AAAAAAAAAAAAAAAAAAAAAAAA 1508
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STREET: 51 University Street
CITY: Seattle
STATE: Washington
                                          ; Sequence 8, Application US, 08300903A; Patent No. 5591630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA UV DOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: 3..E
US-08-300-903A-8
                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                            98101
    RESULT 5
US-08-300-903A-8
                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1417 TGCCACTGTTCTATTCTTTA-AGTATACCTTTCGACTATGTTTTGAAGATGCAACGATAT 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MICTOSOFT WORD FOR Apple OPERATING SYSTEM: Apple OPERATING SYSTEM: Apple OPERATING SISTEMICATION DATA:
APPLICATION NUMBER: US/08/300,903A
FILING DATE: 05-EPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/236,919
FILING DATE: 06-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POEKTAIS, PALTICIA ANNE
REGISTRATION NUMBER: 34,695
REFERENCE/POCKT NUMBER: 2822-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
Sequence 6, Application US/08300903A
Patent No. 5591630
GENERAL INFORMATION:
APPLICANT: Anderson, birk M
APPLICANT: G1ri, Judith G
TITLE OF INVENTION: Inherleukin-15 Receptors
NUMBER OF SUDENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1476 AAAATGAAAAAAAAAAAAAAAAAAAAAAA 1508
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STREET: 51 University Street
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Best Local Similarity 60.89
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
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; LOCATION:
US-08-300-903A-6
                                                                                                                       US-08-300-903A-6
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                    1383 TTGTGTGCATCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTATA 1442
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ROBEY, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILLING DATE: 03-NOV-1989
                                                                                                                                                                                                        Length 1493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1128-A
CURRENT PPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER APPLICATION NUMBER: 08/924,759
SAFTWARE: MICROSOFT WORD VERSION 7.0A
                                                                                                                                                                                                    Score 43.4; DB 6; Length 1
Pred. No. 0.039;
0; Mismatches 66; Indels
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58.7%; Pred. No. 0.05;
tive 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                 1480 TGAAAAAAAAAAAAAAAAAAAAAAAA 1508
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                                                                                                                                                                                                   Query Match 2.9
Best Local Similarity 55.7
Matches 83; Conservative
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APPLICANT: Rothe, Mike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 74; Conserv
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|1053 aaaaaa 1058
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                                                                                                       ; SEQ ID NO:5:
: LENGTH: 1493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-248-335-35
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LENGTH: 1098
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US-08-569-749-1
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2422 AGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTGTTTTAAAATAAGGATTTT 2481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1348 AGAGTCAAGTTTCATTGTAGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTT 1407
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0
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Pred. No. 0.074;
0; Mismatches 74; Indels 0
                                                                                  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
Goeddel, David v
FENTION: INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELEPROCATION INFORMATION:
TELEPRONE: (415,781-1989
TELEPRONE: (415,781-1989
INFORMATION FOR SEQ. ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/569,749
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                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%;
illarity 54.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2589 base pairs
               TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 87; Conserv
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                                                                                                                                                                             COUNTRY:
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1406 TTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGAT 1465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1379 CTTTTTGTGTGCATCAAGTTRCTGTCGTTTTTATGAGTTGCCACTGTTCTATTTAAAG 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.2; DB 3;
Pred. No. 0.074;
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US-08-821-994-64
Sequence 64, Application US/08821994A
Patent No. 6226643
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Greenland, Andrew J
TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-12
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1997-03-18
EARLIER FILING DATE: 1997-03-18
EARLIER PILING DATE: 1996-03-22
SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.8%;
Best Local Similarity 63.1%;
Matches 65; Conservative
                                                                              LENGTH: 1223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-64
                                                                                                                                                                                                                           CDS
55..1223
                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                      55..990
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LOCATION:
                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-154-874-4
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LENGTH: 1474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1408 TTTATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGACTATGTTTTGAAGATGC 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1348 AGAGTCAAGTTTCATTGTAGATCATCGTCCCCTTTTTGTGTGCATCAAGTTTCTGTCGTT 1407
APPLICATION NUMBER: PCT/US96/12860

FILING DATE: 06 AUG 1996

FILING DATE: 06 AUG 1996

RICASSIPICATION: 1996

PRICASIPICATION DATA: 0.S. Serial Nos. 08/512,946 & 08/569,749

CLLASSIPICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749

CLLASSIPICATION NUMBER: 24,774

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION: TELEPHONE: (415)781-1989

TELEPHONE: (415)781-1989

TELEPHONE: (415)398-3249

INPORMATION FOR SEQ ID NO: 1: SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 42.6; DB 5; Length 2589; Best Local Similarity 54.0%; Pred. No. 0.074; Matches 87; Conservative 0; Mismatches 74; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FADER, GARY MICHAEL
TITLE OF INVENTION: ISOFLAVONE BIOSYNTHETIC ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1468 AACGATATAAAATGAAAAAAAAAAAAAAAAAAAAAAAA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITY: MILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERNCE/DOCKET NUMBER: BB-1098-A
TELECOMMUNICATION:
TELEPHONE: 302-992-4926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/931,668
FILING DATE: SEPTEMBER 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09154874
Patent No. 6054636
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2589 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US96-12860-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-154-874-4
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PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1007 MARK
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                        ; ORGANISM: SOYBEAN US-09-247-373B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-296-715-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861 TIAATIGACIGIGATIIGGIIGGGIATIGGCIATIIIAAITITAACIAAAAAAAGIGIIC 920
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GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DAFE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 41.8; DB 3; Length 991; 59.8%; Pred. No. 0.087; tive 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
47; Indels
                                                                          APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENZYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,747
                                                                                                                                                                                            ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
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              Sequence 25, Application US/08924747
Patent No. 6063570
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CL-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302-773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
US-08-924-747-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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US-09-247-373B-25
  US-08-924-747-25
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1392 TCAAGTTTCTGTCGTTTTTATGAGTTGCCACTGTTCTATTCTTTAAGTATACCTTTCGAC 1451
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                                          Gaps
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  DB 4; Length 991;
                                          47; Indels
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANTEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE
TITLE OF INVENTION: ENTYMES
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
Score 41.8; DB 4
Pred. No. 0.087;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 41.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELAWARE: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/296,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CL-1108
                                                                                                                                                                                                                                                                                                              ; Sequence 25, Application US/09296715
; Patent No. 6171839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFRENCE/DOCKET NUMBER: CL-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
  2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 991 base pairs
                     Best_Local Similarity 59.8
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IMMEDIATE SOURCE:
; CLONE: SSM.PK0067.G5
US-09-296-715-25
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                                                                   1392 TCAAGITICIGICGITITIAIGAGIIGCCACIGIICIAIICITIAAGIAIACCTIIICGAC 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                            US-08-197-340-4

Sequence 4, Application US/08897340

Fatent No. 5955306

GENERAL INFORMATION:

APPLICANT: Glmeno, Carlos J. and Errada, Patrick, R.

TITLE OF INVENTION: Weight Control Pathway Genes and Uses

TITLE OF INVENTION: Therefor

NUMBER OF SEQUENCES: 36

CORRESPENDENCE ADDRESS:

ADDRESSE: LAHIVE & COCKFIELD, LLP

STRRET: LAHIVE & COCKFIELD, LLP

STRRET: Boston

STRRET: Massachusetts

COUNTRY: USA

ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 41.8; DB 2; Length 1700;
66.3%; Pred. No. 0.1;
tive 3; Mismatches 25; Indels 0
Best Local Similarity 59.8%; Pred. No. 0.087;
Matches 70; Conservative 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,340
FILING DATE: US/08/897,340
FILING PAPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/715,032
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
WANDE: CALLOST ADAR ANDER: US/08/715,032
FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 39,030
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-005CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1486 AAAAAAAAAAAAAAAAAAA 1508
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Best Local Similarity 66.34
Matches 55; Conservative
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US-08-897-340-4
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Search completed: November 5, 2001, 18:04:56 Job time: 15096 sec

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em_esthum15: em_esthum17: em_esthum17: em_esthum17: em_esthum19: em_esthum21: em_esthum22: em_esthum22: em_esthum24: em_esthum24: em_esthum24: em_esthum26: em_esthum26:

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(without alignments)
2450.648 Million cell updates/sec
                                                            November 5, 2001, 18:00:56 ; Search time 5816.79 Seconds
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                     10228115 seqs, 4726426750 residues
                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                            OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                    Scoring table:
                                                                                                                                                                     Database :
                                                                          Sequence:
                                                                                                     Searched:
                                       Run on:
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em_estov2:*
em_estp11:*
em_estp12:*

em_estpl3:*

em_estin2:* em_estin3:* em_estin4:*

em_estoml:* em_estom2:* em_estov1:*

em_estin5

em_estpl4:*
em_estpl5:*
em_estpl6:*
em_estpl7:*

em_estp11.0:*

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em_estro10:*

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em_estro15:*

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117: 9p_cet48:*
119: 9p_cet48:*
120: 9p_cet51:*
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122: 9p_cet52:*
123: 9p_cet52:*
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127: 9p_cet52:*
128: 9p_cet62:*
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140: 9p_cet62:*
140: 9p_cet62:*
150: 9p_cet62:
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em_gss_other:*
em_gss_pln1:*
em_gss_pln2:*
em_gss_pro:* gb_gss31:*
gb_gss32:*
gb_gss33:*
gb_gss33:*
em_gss_inv4:*
em_gss_rod6:*
em_gss_rod6:* em_gss_fun:* em_gss_huml:* em_gss_hum2:* em_gss_hum6:* em_gss_hum7:* em_gss_hum8:* em_gss_hum9:* em_gss_inv1:* em_gss_inv2:* em_gss_inv3:* em_gss_rod1:* em_gss_rod2:* em_gss_rod3:* em_gss_rod4:: em_gss_rod5:: em_gss_vrt2:: em_gss_vrt2:: em_gss_vrt3:: gb_gss1:: gb_gss1:: em_gss_rod8:* gb_gss35:* gb_gss36:* gb_gss37:* em_gss_hum3:* em_gss_hum4:* em_gss_hum2:* gb_est110:*
gb_est111:*
gb_htc:* gb_gss11:* gb_gss12:* gb_gss13:* gb_gss28:* gb_gss29:* gb_gss30:* gb_gss4:* gb_gss5:* gb_gss6:* 9b_9ss17: 9b_9ss18: 9b_9ss19: 9b_9ss20: 9b_9ss21: 9b_9ss22: gb_gss24:: gb_gss25:: gb_gss26:: gb_gss27:: gb_gss7:*
gb_gss8:*
gb_gss9:*
gb_gss10: gb_gss14: gb_gss15: gb_gss16:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Anote—"Vector: Bluescript SK(-); Site_1: BcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers." ä TITAATAAAAAACCAGAAATAAAACACGTTGAAGGTGATTCTGTTGTGGTTACTTTTGCA 320 380 353 381 TATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGATTGCGTCACGGTCCCA 440 441 CTTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATCACTAGGAATGACGAAT 500 81 ATTACTEGGCFACTCTTCCCFCCGGTCCACCATCTTTTCTTCTATGACTTTCCACATTCT 140 CATGITITGGTFAGGGTTCCACCGTATACGGCGGGATATTATTCTACAAGCTCCCCATTTC 128 CATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAAAGGGTGGACTTCGATT 560 Gaps 21 CGAATATCGGCCCCCTCGGi3CACCATCGGCCATCGCTCGTTATCTTACTTTCTTCGAC 80 Research Genetics, Libraries 9 CAAGTTGCGCCACCTCCGGGCGGCGCGCGGGGGGGCGCACTCCCTCTTACTTTTGAT 242 -----ATATCCTGAGTIACATTATGTGACAGGAGATTCTGTATCTGTTACTTTTTCT 141 AAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAATCTTTATCGGTCACTCTT 321 GAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCTCGAAAATGTGAAAACTTT CAACATTTTTCCCGTTTGCTAGTAATTTGATTGTATTTCCTAACACTGATGGTTCGGGT 189 AAACACTATACGCCCTTAGCTGGAAACGTTGCTCGTCCACTAGATACAAACGG-----561 ATTCAATCTGGTGTAGATCGGTCTTTTTAACGAAAGGATCTCCACCGGTTTTTGATAG Score 130.2; DB 155; Length 690; Pred. No. 6e-21; 0; Mismatches 268; Indels 15; /organism="Solanum tuberosum"
/cultivar="Rennebec"
/db_xrefe"taxon:4113"
/clone='cSTS55122"
/clone_lib="cSTS"
/tissue_type="Sprouting eyes from tubers"
/dev_stage="l2-14 weeks post harvest"
/lab_host="SOLR" Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, I
Division tel 1.800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.

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BGS91758 763 bp mRNA EST 12-APR-2001
EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone
BPLI10A14 5' sequence, mRNA sequence.
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                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasteridas I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 763)

Zhang, P., Hennandez, M., Tornqvist, C.-E, Wirtz, U., Loukoianov, A., Rangel, P., Haberlach, G.T., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.M., Helgeson, J. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans. Incompatible Reaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 ACACTGATGGTTCGGGTTTTAATAAAAACCCAGAAATAAAACACGTTGAAGGTGATTCTG 303
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                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 TATCTGTTACTTTTTTGAGACTGATATGGATTTCAATTATCTCATTGGTGACCATCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%; Score 124.4; DB 155; Length 763; 53.2%; Pred. No. 1.5e-19; 1ve 0; Mismatches 246; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="P, infestans-challenged leaf"
/tissue_type="leaf"
/dev_stage="6 week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPL110A14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                               BG591758.1 GI:13609898
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162 c
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                                                                                                                                               Solanum tuberosum
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and effectilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sateridae; euasteridas; Solanales; Solanaceae; Solanum.

(bases 1 to 570)
van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J., Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potato leaves and petioles Solanum tuberosum cDNA clone
GGGTCCAATTAGCTCCGGTCTTAGCCATTCAAGTGACACTTTTTCCGAATCTTGGTGTAT 452
                                                                                                                                                                                                         CACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGA 543
                                                                                                                                                                                                                                                                   453 CCATTGGTTTCACTAACCATCATGTTGTTGGTGATGGAGCTACCATAGTAGGGGTTCATTA 512
                                                                                                                                                                                                                                                                                                                              544 AAGGGFGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTAACGAAAGGATCTC 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Rouning
The Institute for Genomic Research
For clone request: please contact Research Genetics,
Division Let 1-800-711-6195, email cdna@resgen.com.
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/clone_lib="potato leaves and petioles"
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/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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    570
    /organism="Solanum tuberosum"
/cultivar="Kennebec"

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VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
Estaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta: Magollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                 271
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                                                                                                                                                                                                                                                                                                                                                                      484
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTAGGAATGACGAATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTACTTATTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATATTATTCTA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESTs from uninoculated seedling roots of Medicago truncatula Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pKV0-1613, mRNA
                                                                                                                                                                                                                                                    317 ATCTGTTACTTTTTCTGAGACTGATATGGATTTCAATTATCTCATTGGTGACCATCGGG
                                  TGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAATC
                                                CAAGCTCCCCATTCCAAACCCGATTCGTTCAAAAATTC
                                                                                                 185 TITAICGGICACTCTICAACAITITITCCCGTTTGCTAGTAATTTGATTGTATTTCCTAA
                                                                                                                    272 TACAAACGG------ATATCCTGAGTTACATTATGTGACAGGAGATTCTGT
                                                                                                                                                                                                                                    TGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCTCG
                                                                                                                                                                                                                                                                                                    AAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGA
                                                                                                                                                                                                                                                                                                                                                                      TTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATATC
                                                                                                                                                                  CACTGATGGTTCGGGTTTTAATAAAAAACCCAGAAATAAAAACACGTTGAAGGTGATTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE187619 788 bp mRNA EST
EST335180 KVO Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: Skmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
1. .788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tal: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: kate@mail.bio.tamu.edu
Texas A&M University name:T260795e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR sequence name: MTGAU50TK More information is available at. http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="pKV0-1613"
/clone_llb="KV0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BE187619
BE187619.1 GI:8666803
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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RESULT

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/tissue_type="Seedling roots"
//de_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
//dab_host="E.coli strain xLOLR"
//dab_host="E.coli strain xLOLR"
//note="Vector: pBluescript SK -; Site_l: EcoRI; Site_2:
Xhoi: JONA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
37 a 188 c 100 g 262 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ς,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE920468 575 bp mRNA EST 02-0CT-2000 EST424237 potato leaves and petioles Solanum tuberosum cDNA clone correct sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 ------CGTTCCCTCGCTTGATCTAACCGAACCTCAACTCGAATTTACTCTTAAC 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 TCATTTGAAGTAAAAAGAGTTCCCTTTGTTAGCTATTCAAATAACATCCTTCCCAAATTAT 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 TCGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 TICITCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 TACTCAAGAGATGTTAATGATTCCACCCTTTGGTACCAAAGTTGCAACA---AATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 AACTCGGTTTCATTCACGGICGCAGAGTCAAATAGCGACTTTGAACACTTGTGCTCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 TTTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 110.2; DB 164; Length 788;
Pred. No. 3.9e-16;
0; Mismatches 213; Indels 21;
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                                                ACCESSION
                                                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                     AUTHORS
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                                                                VERSION
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                                                                                                                                                                                                                                           /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol: Tissue was supplied by Dr. Fry (Cornell University). Leaflets and perioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in limit in thoom.
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                                                                Libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGATCTCGTCTTGATCCACCAATTCCCACAGCCTACTTTGGTAACTGTGGTGCACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 142; Length 575;
 Generation of ESTs from potato leaves and petioles Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Score 107.6; DB 142; Length
Pred. No. 1.6e-15;
0; Mismatches 239; Indels
                                                                                                                                                                                 /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/tissue_e="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                          /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                     /cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB6C8"
                                                                                                                                                                                                                                                                                                                                   139 g
                                                                                                                                                                                                                                                                                                                      liquid nitrogen
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53.88;
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Best Local Similarity 53.8
Matches 299; Conservative
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1 (bases 1 to 487)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang
,F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tankaley, S.D.
Generation of ESTs from wild tomato (Lycopersicon hirsutum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Pred. No. 1.9e-15;
0; Mismatches 193; Indels
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Contact: David Frisch
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 1864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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/clone="cLHT1D15"
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/cultivar="TA496" |
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/clone_lib="toxon:4081"
/clone="toxon:4081"
/clone="to
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Contact: David Frisch
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                    AW221049 606 bp mRNA EST 07-DEC-1999
SET297318 tomato fruit mature green, TAMU Lycopersicon esculentum
CDNA clone cLEF3F1, mRNA sequence.
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3 AACATTCTCGAACATGCCCGAATATCGGCCCCCTCGGGCACCATCGGCCATCGCTTA
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Pred. No. 2.2e-15;
0; Mismatches 280;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
TTE: 864 656 4366
Fax: 864 656 4293
                                                                                                                      441 CCATTGGTTTCACTAACCATGATGTTGTTGTGGTGATG 476
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Best Local Similarity 50.4%;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

I (bases I to 508)

S van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tankaley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles

Unpublished (2000)

Contact: Cathy Ronning

The Institute for Senomic Research

For clone info: please contact Research Genetics, Libraries

Division tel 1-800-711-6195, email cdna@resgen.com.
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                                                                                                                                                                                                                       GTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATCATCCT 362
                                                                                                                                                                                                                                                                363 CGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGT 422
                                                                                                                                                                                                                                                                                                                                                                                      415 GGGGTCCAACTAGCCCCCCTCTTAGCCATTCAGGTGACACTTTTTCCGAATCTTGGTGTA 474
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                                                                                                                                                       250 GATACAAACGGAT------ATCCTGAGTTACGTTATGTGACAGGAGATTCT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGGGTATA
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/db_xref 'taxon:4113"
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               106
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                                                                         6.9%;
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              123 c
                                                                                       Best_Local Similarity 52.5
Matches 286; Conservative
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1 (bases 1 to 574)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Lilang, F., Cho, J., Utterback, T., Hanssen, C.L., Doan, B., Bouger, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                      AACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTGTAT 237
                                                                                                                                                                                                                                                                     ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATC 357
                                                                                                                                                                                                                                                                                                   335
                                                                                                                                                                                                                                                                                                                               358 ATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAAT 417
                                                                                                                                                                                                                                                                                                                                                                                          477
                            TCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAA 177
                                                                                                                                                                                                          238 TTCCTAACACTGATGGTTCGGGTTTTAATAAAAACCAGAAATAAAACACGTTGAAGGTG 297
 Gaps
                                                                                                                                                                                                                                       CACTAAATTCGAGTGGTT-------ATCCTGAGTTGCGTTATGTGACTGGAG
                                                                                                                                                                                                                                                                                      TATGTGATTGCGTCACGGTCCCACTTTTTCACTTCAAGTGACGTTTTTTCCGGGCTCGG
 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCAC 526
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
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BE922746.1 GI:10448822
 Conservative
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Solanum tuberosum
252;
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGATTCTATATCTCTTTATTGAGACTGATATGAATTTCAATCATCTCATTGGTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 ATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTITITGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATTCATAAGAACATGGGGTTTACTCAACAAATTCGGCGGTGATGAACAGTGCTTAGAGA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGATCTCCACCGGTTTTTGATAGATTGATTAACATCCCACATTTAGATGAAATAAGT 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 GTCCACTAAATTCGAGTGGTT------ATCCTGAGTTGCGTTATGTGACTG 187
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                          23 TTTTATTCTACAAGCTACCAATTTCCAAACTCGATTTCGTTCAAACCATTATTCCTACTC 82
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                                                                                                                                                                                          18;
                                                                                                                             Length 574;
                                                                                                                         Score 103.4; DB 142; Lengt
Pred. No. 1.6e-14;
0; Mismatches 241; Indels
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Clemson University
183
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AW221050
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l (bases 1 to 591)
Jaclaid, Vreballov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG15H6, mRNA sequence.
BE434257 GI:9432100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 TTTTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCAGGC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAAACAATCTTTATCGGTCACTCTTCAACATTTTTTCCCGTTTGCTAGTAATTTGATTG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 TTAAAAATTCACTCTCCCTCACTCTCAAACACTATACGCCCTTAGCCGGAAACGTTGCTT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 GTCCACTAGATACAAACGGAT ------ATCCTGAGTTACGTTATGTGACAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 ATCATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 TATTATTTTACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                      Spermatophyta; Maynollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of EST: from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 TATTTCCTAACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAAACGTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATCCGCGTAAGGCTAAGGATTTTTATCACTTTGTTCCTAAGTTAGGGGAACCTAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_nost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 167;
Pred. No. 1.8e-13;
                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 436
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4081"
/clone="cLEG15H6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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illarity 51.7%;
Conservative
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                                                                                                  tomato.
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                                      ACCESSION
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                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                     /note-vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; cLEF - Fruit were tagged at the lom stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTTTCTTC 122
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                                                                                                                                                                    /db_xref="taxon:4081"
/clone="cLEF3F3"
/clone="Lb="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 113; Length 583;
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/organism="Lycopersicon esculentum"
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0; Mismatches 278;
  100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                              Location/Qualifiers
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                Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                  /cultivar-"TA496"
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Matches 295; Conservative
                                                                            prime sequence.
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Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Journal Poly, E.D.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Mol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and perioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Steridae; euasterida I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 564)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
                                                                                                                                                                                                                                                                  564~\rm bp mRNA EST 02\text{-}OCT\text{-}2000 potato leaves and petioles Solanum tuberosum cDNA clone 5' sequence, mRNA sequence.
                                   421
                                                                                         118 TCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 CGGGTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 CGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTTT 117
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                    535 ACTITITGAAAGGGTGGACTTCGATTATTCAATCTGGTGTAGATCGGTCTTTTTTAACGA
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/tissue_type-"leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_nost="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB13B18"
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BE921494.1 GI:10447486
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Solanum tuberosum
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Matches 265;
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/note="Vector: pBluescriptSKmcUdadapt; Site_1: 5' EcoRI; Site_2: 3' XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 482)
van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST400516 tomato nutrient deficient roots Lycopersicon esculentum cDNA clone cLEW18020 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                      359 ATCCTCGAAATGCTAAGGATTTTTATCCCATT---CCTCAATTGGCACAACCTAAGGATG 415
                                                                                                                                                                                                                                358 ATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAAT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476 GCATATCCGTTGGTTTTAGTAACCATCATGTCGCTTGTGAAGGAAATACCATCGTGAAAT 535
                                                                                               ATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAATC 357
299 ATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTCAATCATCTCATTGGTAACC
                                                                                                                                                                                                                                                                                                                                                                                             478 GTATATCACTAGGAATGACGAATCATCATAGCCTTGGTGACGCTAGCACGCGGTTCAACT
                                                                                                                                                                                                                                                                                                                                                           418 TATGTGATTGCGTCCACGTCCCACTTTTTTCAAGTGACGTTTTTTCCGGGCTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation of ESTs from tomato nutrient-deficient roots
Unpublished (1999)
Contact: David Frisch
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/tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
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/clone="cLEW18020"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538 TTTTGAAAGGGTGGACTT 555
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DB 144; Length 482;

Score 92.6;

5

ò d ò g õ g ò q ò g ò g ò g

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/dev_stage="effective root nodules harvested one month post inoculation with Sinorhizoblum melilot!"
/lab_host="E. col1 strain xLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; cNNA was prepared from poly4+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizoblum meliloti. The cDNA was directionally liqated into the Uni-zAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon.
1 (bases 1 to 497)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW930934 497 bp mRNA EST 30-MAY-2000 EST356777 tomato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF42M23 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 TTATGTGATTGCGTCACGGTCCCACTTTTTTCACTTCAAGTGACGTTTTTTTCCGGGCTCG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGTTATCTCTTACTTTCTTCGACATTACTTGGCTACTCTTCCCTCCGGTCCACCATCTT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTTCTATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 CCTCATGA-------TTCTCACAAGCCAATCATTAAATTCATAAAGGA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 GATTCTGTTGTGGTTACTTTTGCAGAATGTTGTCTTGACTTTAATAATTTGACAGGAAAT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCCTCGAAAATGTGAAAACTTTTATCCACTTGTACCTTCATTGGGAAATGCAATCAAA 416
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                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                   Length 630;
                                                                                                                                                                                                                                                                                                                                                               Score 91.4; DB 155; Length
Pred. No. 1.2e-11;
0; Mismatches 201; Indels
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llarity 53.1%;
Conservative
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Best Local S
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Sosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 630)
Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Minnesota name: M382308e TIGR sequence name: MTCDG96TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG581249 630 bp mRNA EST 11-APR-2001
EST482982 GVN Medicago truncatula cDNA clone pGVN-64023 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 truncatula, 2001
Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 17el: 612 625 5715
Fax: 651-649-5058
                                                                        CTCTTACTTCTTCGACATTACTTGGCTACTTCCTTCCGGTCCACCATCTTTTCTTCT 123
                                                                                                                 CTCTTACTTATTTTGACCATGTTTGGTTAGGGTTTCGCCGTATGAGGCGGGTATTTTT 109
                                                                                                                                                              124 ATGACTTTCCACATTCTAAATCCCATTTCATGGACACTATTGTTCCCAGGCTAAAACAAT 183
                                                                                                                                                                                                          ACAAGCTCTCCATTTTCAAACCCGATTTCGTTCAAAACATTATTCCTCCTCTTAAAAATT 169
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                            ACACTGATGGTTCGGGTTTTAATAAAAAACCAGAAATAAAAACACGTTGAAGGTGATTCTG
                                15;
                                Indels
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/clone_1ib="gGVN"
/tissue_type="N2-fixing root nodules"
      Pred. No. 6.2e-12;
0; Mismatches 194;
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTAGGAATGACGAATCATCAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG581249
BG581249.1 GI:13596313
      52.8%;
                           Matches 234; Conservative
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         Best Local Similarity
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VERSION
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Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verlify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 CCACTTGTACCTTCATTGGGAAATGCAATCAAATTATGTGATTGCGTCACGGTCCCACTT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 AATAAAAACCAGAAATAAAACACGTTGAAGGTGATTCTGTTGTGGTTACTTTTGCAGAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 IGTIGICITGACTITAATAATTIGACAGGAAATCATCCTCGAAAATGTGAAAACTITTAT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 CATAGCCTTGGTGACGCTAGCACGCGGTTCAACTTTTTGAAAGGGTGGACTTCGATTATT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 CACTITGTTCCTAAGTTAGGGGAACCTAAGGATGCACCGGGGGTCCAACTAGCCCCGCTC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 CATGITGITGGTGATGGAGCTACTATAGCAGGGTTCATTAAGGCGTGGGCTCTACTCCAC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AAATICGGIGGACATGAACAATICTTAICGAATGAGCTAATTCCATTTTATGATAGGT 425
                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 89.2; DB 122; Length 497; 53.1%; Pred. No. 4.1e-11; tive 0; Mismatches 168; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEF42M23"
                                                                                                 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4236
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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                                                                                                                                                                                                                                      Location/Qualifiers
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                                                            Unpublished (1999)
Contact: David Frisch
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106 c
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Matches 190; Conservative
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Search completed: November 5, 2001, 18:01:00 Job time: 14900 sec

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_htg23:*
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2643.712 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                1344157 segs, 7733874588 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
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Listing first 45 summaries
                                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
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E12753 Gentianatri E12757 Senecio cru E12754 Gentianatri AB026494 Gentiana AB016892 Arabidops

E12753 E12757 E12754 AB026494 AB016892

1200112

E12756 Perilla oci AB029340 Perilla f AB010708 Gentiana

E12756 AB029340 AB010708

qi

Description

SUMMARIES

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AE001425 Plasmodiu
AX015915 Sequence
AF30506 Dictyoste
AC069470 Arabidops
AF310896 Dictyoste
X77854 P. Falciparu
AC026290 Homo sapi
                                                                                                                                                                                                                                                                              AJ05398 Dictyoste
AB028618 Arabidops
AL425357 clone BA0
M23449 Dictyoseliu
Continuation (4 of
AF337815 Dictyoste
                                                                                                                                                                                                                                                                                                                                                                           AL109814 Plasmodiu
AC004153 Plasmodiu
AC024245 Homo sapi
X54161 D discoldeu
U53326 Plasmodium
AC010933 Homo sapi
                                                  AC069470 Arabidops
AX025514 Sequence
                                                                                AL427102 clone BA0
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D13973 Dictyostell
AC005140 Plasmodiu
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AL035477 Plasmodiu
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AL427351 clone BAO
AF310894 Dictyoste
                                     Arabidops
                                                                                                    AP000606 Arabidops
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                                   AB028618
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PFMAL13PB
AC004153
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DDMYOSLC
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AF310896
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CNS071TJ
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AC069470
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AP000606
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AE001425
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AF310893
DDIDP87
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CNS07A6G
CNS073CX
AF310894
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83
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4.6 82360
4.6 341064
4.3 224448
4.1 11829
4.1 49999
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1.0 1741
1.0 136047
1.0 4596
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ALIGNMENTS

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NAKAO
                                                                                                                                                                                                                                                                               FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
                                                                                                                                                                                                                                                196915 PI
                         24-JUN-1998
                                                                                                                                                                      Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y., Yonekura,K., Mizutani,M. and Kusumi,T. GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY PATANT. JP 1997070290-A 4 18-MAR-1997;
                                     acyltransferase, partial cds
                                                                                                                                                                                                                                                                                                                  (C12N9/10,C12R1:19);
strandedness: Double;
topology: Linear;
Key
                 Perilla ocimoides mRNA
E12756
                                                         E12756.1 GI:3251588
JP 1997070290-A/4.
unidentified.
                                                                                                           unclassified.
1 (bases 1 to 1479)
                                                                                               unidentified
                                                                                                                                                                                                                                                                                                        C12R1:865),
                                                                                                                                                                                                                                                                                                                     200
                                 DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                 SOURCE
ORGANISM
                                                                                                                      REFERENCE
                                                                                                                                                                      JOURNAL
                                                                                                                                   AUTHORS
                                                                                                                                                         TITLE
RESULT
E12756
                                                                                                                                                                                              COMMENT
                        LOCUS
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TGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCG 367
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                                                                                                                                                                                                                                                                                             ACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAAT 187
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           FT
           ocimoides'
                                                                                                               others
                                                                                                                                                        Score 765.4; DB 10; Length
Pred. No. 2.5e-147;
1; Mismatches 417; Indels
                                                     /product='acyltransferase'
          /organism='Perilla
                                /clone='psaT208
                                                                                                              411
                                                                 Location/Qualifiers
1. 1479
/organism="unidentified"
                                                                                                 /db_xref="taxon:32644"
316 c 331 g
                                            . .1343
                      /tissue_type='leaves
                                                                                                                                                        Query Match 50.3%;
Best Local Similarity 71.1%;
Matches 1056; Conservative 1
 source
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Ashikari, T., Yamaguchi, M. and Kusumi, T.
Molecular and blochemical characterization of a novel
Molecular and blochemical characterization of a novel
hydroxycinnamoyl-CoA: anthocyanin 3-0-glucoside-6
L. Unpublished (1999)
E. 2 (bases 1 to 1476)
Sakakibara, K.Y. and Tanaka, Y.
Direct Submission
Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko Y.
Sakakibara, Sundcy Research Center, Fundamental Research, Plant
Biotech; Shimamoto-cho, Wakayamadai, 1-1-1, Mishima-gun, Osaka
618-6503, Japan (E-mali:Relko_Sakakibara@suntcry.co.jp,
Tel:+81-75-962-8807, Fax:+81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perilla frutescens leaf cons.
Perilla frutescens leaf cons.
Perilla frutescens
Eukaryota: Viridiplantaes: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Lamiaceae; Perilla.
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Perilla frutescens mRNA for anthocyanin acyltransferase, partial
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                                                                                                                                                                                                                                                                                                                    CGGTGGAGAAATGGTCGCCGGAGATTCGTAAAGCGTTGCAGAAATCATATTTTCGGTGG 1134
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                  CGTACGCGCTGCCGAGAATGCGGCGGCGGAGAGCTGGTGGTGGGAGAGAAAGGGGGTGTTTCTGG
                                                                                                                                                                                                                             CAGCTGAGGCGATCGCGGGGAAATAGAGAAGAGGACGAGGACGAGAAGATTCTAGAAA
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                                                                                     TCGATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTAT
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/Transletion-"VIECRNGPPDSVAEQSVPLTFFDMTWLHFHPMLQLLFYEFPC
SKQHFSES IVPKLKQSLSKTLIHFFPLSCNLITPSSPEKMPERFYLSGDSVSFTIAES
SDDFDDLYGNRPESPVRINTNPVRLPPLYESDRKLEQVFAVQYTFPGRGVGIGTAT
HHTVSDAESFLARFITNRVPKLPPLTENEDEDEEFKSLPVFDRSVIKYPTKFDSITWRNA
LKFPLQSRHPSLPTDRIRTTFVFTQSKIKKLKGWIQSRVPSLVHLSSFVAIAAYWARG
ITKSFTADEDQUNEDAFFLIPVDLRPRELDPPVPENYEGNCLSYALPRHRRELVGEKG
VFLAAEVITAAEIKKRINDRKILETVEKWSPEIRKALQKSYFSVAGSSKLDLYGADFGW
GRARKQBILSIDGSKAMTLCKARDFEGGLEVCLSLFKDKMDAFAAVFSLGING"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CTCTCTCTAAAACTCTCATACACTTCTTCCCTCTCTCATGCAATTTAATCTACCCTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 TGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CAGAATCTAGCGACGACTTCGATGATCTCGTCGGAAATCGTCCAGAATCTCCCGTTAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 ACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 AAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGGTGTGCATCGGAATAACGA
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9
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                                                                                                                                                  /product-"anthocyanin acyltransferase"
/protein_id-"BAA93475.1"
/db_xref="G1:7415646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.2%; Score 763.6; DB 12; 70.5%; Pred. No. 6e-147;
                                        /organism="Perilla frutescens"
/db_xref="taxon:48386"
/tissue_type="leaf"
Location/Qualifiers
                                                                                                                                   /codon_start=3
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FPNRGIAVALTAHHSIADAKSFVWFINAWAYINKFGKDADLLSANLLPSFDRSIIKDL
SCLEETFWANDRAVDLEHFSRFGSKPPRFNKVRATYVLSLASIOKLKNKYLNLRGSBPT
IRVITFTWTGRYWTCWNK KRODVSEESSNDENELEYSFTADCRGLLTPPEPPNY
GNCLASCVAKATHREGYWTCWAYAAIGEAIEKRLENEKGYLADAKTWLSENGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEQIQMVKVLEKCQVTPPSDTTDVELSLPVTFFDIPWLHLNKMQ
SLLFYDFPYPRTHFLDTVIPNLKASLSLTLKHYVPLSGNLLMPIKSGEMPKFQYSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDSITLIVAESDQDFDYLKGHQLVDSNDLHGLFYVMPRVIRTMQDYKVIPLVAVQVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AAGATGCAGTCCCTTCTGTTTTACGACTTTCCGTACCCAAGAACACATTTCTTGGACACT 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCG 396
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                                                                                                                                   cDNA cloning, gene expression and subcellular localization of anthocyanin 5-aromatic acyltransferase from Gentiana triflora Plant J. 16 (4), 421-431 (1998)
(E-mail:Hiroyuki_Fujiwara@suntory.co.jp, Tel:+81-75-962-8807 Fax:+81-75-962-8262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAGTTCCGGTA----TCAG
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                                                                                                                                                                                                                                                                                                                                                                                                 /product="Anthocyanin 5-aromatic acyltransferase"
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/db_xref="GI:4185599"
                                                 2 (sites)
Fujiwara,H., Tanaka,Y., Yonekura-Sakakibara,K.,
Fukuchi-Mizutani,M., Nakao,M., Fukui,Y., Yamaguchi,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1679;
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Pred. No. 1.1e-29;
                                                                                                                                                                                                                                                                    /organism="Gentiana triflora"
/db_xref="taxon:55190"
/clone="pGAT4"
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6. .1415
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51.2%;
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Fujiwara, H., Tanaka, Y. and Kusumi, T.

Fujiwara, H., Tanaka, Y. the DDBJ/EMBL/GenBank databases. Submitsed (22-JAN-198) to the DDBJ/EMBL/GenBank databases. Hiroyuki Fujiwara, Suntory LTD., Inst. of Fundamental Research; 1-1-1, Wakayamadai, Shamamoto-cho, Osaka 618-0024, Japan
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Gentiana triflora mRNA for Anthocyanin 5-aromatic acyltransferase,
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                                                    CGTTTGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGG
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                                                                                                                 ATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCGGCATCGCCA
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Gentiana triflora petal cDNA to mRNA, clone:pGAT4.
Gentiana triflora
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FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 TGCAATCTAATCTACCCTCTNTCGCCGGGGAAAATGCCGGAGTTCCGGTA...--TCAG 279
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                                                                                                                  PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691!
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 GAGGGCGACTCGATAACTTTCATCGTTGCGGAGTCTGACCAGGATTTTGACTACCTTAAA
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GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY PALENT: JP 1997070290-A 1 18-MAR-1997; SUNTORY LTD
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Pred. No. 1.1e-29;
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    1703
    /organism='Gentianatriflora'
    /vartety='Japonica'
    /tissue_type='petal'
    /clone='pGAT4'

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/organism="unidentified"
/db_xref="taxon:32644"
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                                                           Gentianatriflora
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   GGCCTAGAGGAAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTT
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                                                             TTGGACGGAAAAGGTGAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCT
                                                                                                  TTGTCCGCGA-----ATCTTCTTCCATCTTTCGATAGATCGATAATCAAAGATCTGTAT
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1 (bases 1 to 1703)
Ashikari T., Tanaka Y., Fujiwara, H., Nakao, M., Fukui, Y.,
Yonekura, K., Mizutani, M. and Kusumi, T. .
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                                                                                                GGCCTAGAGGAAACATTTTGGAACGAAATGCAAGATGTTCTTGAAATGTTCTCTAGATTT 722
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                                                                                                                                                                                                                                        537 AAATTGGACACATATTTATGGAACAACGCGCAGAAACGTC------CGTTGGAATCG
                                                                                                                        903 GTCGTATCAGAGGAATCATCGAACGACGAAAATGAGCTCGAGTACTTCAGTTTTACAGCG
                                                                                                                                                                                                                                                                                                                      GATITAAGGCCGCGTTTGGATCCGCCGCCTCCGGGGAACTACTTCGGAAACTGTCTATCG
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                       TTGGACGGAAAAGGTGAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCT
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Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
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Senecto cruentus mRNA fi
E12757 1 GI:3251589
JP 1997070290-A/5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 TCGCCGG-------AGAAAATGCCGGAGTTCCGGTATCAGAACGGTGACTCG
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    1508
    /organism="unidentified"
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NAKAO

F

/organism='Gentiana triflora'

/variety='japonica'

Location/Qualifiers

strandedness: Double; topology: Linear; (C12N9/10,C12R1:19);

196915 PI

(bases 1 to 1522)

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PI FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
C12R1:865),
                                                                                                                              OS Gentianatriflora
PN JP 1997070290-A/2
PD 18-MAR-1997
PF 30-JAN-1995 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
                                                            Ashikari, T., Tanaka, Y., Fujiwara, H., Nakao, M., Fukul, Y., Yonekura, K., Mizutani, M. and Kusumi, T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY PATENT: JP 19970;0290-A 2 18-MAR-1997;
 JP 1997070290-A/2.
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                                                                                                     TTGAGACATACAAGGCTCGAAAGTTTTTATAAACCTTCGAGCCTTGTTGGTCCCACTGAT
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                                                                                                                                                                                   CAGAGAAAAGCCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGGATCGCAGCTTATATC
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                          GAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATAT
                                               GGATCTCCACCGGTTTTTGATAGATTGATT - - - AACATCCCACATTTAGATGAAATAAG
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                                                                                                                                                                                           Length 1622;
                                                                                                                                                                                           Score 153.8; DB 10; Length
Pred. No. 1.2e-21;
0; Mismatches 652; Indels
                            35. .1474
/product='acyltransferase'
/tissue_type='petal'
/clone='pGAT106'
                                                                                                                            477
                                                                           1. 1622
/organism="unidentified"
/db_xref="taxon:32644"
1 345 c 322 g 47:
                                                              Location, Qualifiers
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10.1%;
Best Local Similarity 49.4%;
Matches 692; Conservative (
                                 CDS
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24-JUN-1998

E12754 1622 bp DNA PAT 24-JU Gentianatriflora mRNA for acyltransferase, complete cds. E12754 GI:3251586

LOCUS DEFINITION ACCESSION VERSION

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                                                                                                        GCTICCATCACTAAATICGGAGGAGATGATGAATICTIGGACGGAAAAGGIGAAIGTITG 600
                                                                                                                                     GTTTTGGTTGACAAATCCAATGGAGATTC---ATTAAAGTTCCTTCCACTTTCTTCTTA 649
                                                                                                                                                                    CCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATATTTATGGAAC 660
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                                                                                                                                                                                                                                                             710 GAAAGAAAACTGCTCAAAATCTCAGGGCACACCTACTGTTCTAAATCCAGCAATTTCTAAA 769
                                                                                                                                                                                                                                                                                          GATCGGATTCGAGCTACCTATCTACCCAATCTGAAATTAAGAAATTGAAGGGTTTG 768
                                                                                                                                                                                                                                                                                                                        GATGAAGTICGAGCCACCTICATCCTACACCCTATTGATATCATGAAGCTCAAGAAATIC 829
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CCGCCCCGATCAACATCTGCGGCACCAAGGTCGACGCTCATTTATGTCGTTGGATCCGCA
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                                             ATAACGACGCACCACCACTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGG
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AB026494 1622 bp mRNA PLN 04-APR-2000 Gentiana triflora GAT106 mRNA for acyltransferase homolog, complete cds.

LOCUS DEFINITION

RESULT AB026494

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HLHFYRERHPCONSKETISSIKSSLSIVIKHFLDLAGNLIMPDDSSDRMPELBYKKGD
SVSLTIAESSMDFDYLAGDHQRDSYKFNDLIPQLPEPIVTSGDEVLPLFALQVTVFSN
TGCICGRALHAGVLAGASSLFHNKLWAVLDKSGNGSLKKFLDLSLPMYDSSYDDPFH
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APRSTLIYVGSAQRNVHDFDBADFGWGKLEKHESVSTNPSATLILISRSRRFKGALEL
GISLDRNRMDAFATTTNFINSHTNFKLENSTNFKGALEL
322 9 477 t
                                                                                                                                                                                                                                                                                                        frutescens and diverse plant acyltransferase homologs
Unpublished (1999)
2 (bases I to 162)
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5 (bases I to 162)
6 (21-APR-1999) to the DDBJ/EMBL/GenBank databases.
7 (bashikazu Tanaka, Suntory Ltd., Institute for Fundamental Research; Wakayama-dal 1-1., Shinamoto, Osaka 618-8503, Japan
(E-mail:Yoshikazu_Tanaka@suntory.co.jp, Tel:81-75-962-8807,
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                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Gentianaceae; Gentiana.
                                                                                                                                                                                            Yonkura-Sakakibara,K., Tanaka,Y., Fukuchi-Mizutani,M.,
Fujiwara,H., Fukui,Y., Toshihiko,A., Yamaguchi,M. and Kusumi,T.
Molecular clonding and blochemical characteization of
hydroxycinnmamoyl-coa, anthocyanin
3-O-glucoside-6-O-hydroxycinnamoyltransferase from Perilla
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/protein_id="BAA93452.1"
/db_xref="GI:7415597"
                                         acyltransferase homolog.
Gentiana triflora cDNA to mRNA.
Gentiana triflora
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35. .1474
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/gene="GAT106"
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The software programs used to predict genes include: Grall (Informatics Group, Oak Ridge National Laboratory, http://compbio.orml.gov/Grall-1.3/), http://compbio.orml.gov/Grall-1.3/), GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), GENSCAN (Chris Burge, MIT, http://crompio.orml.gov/Grall-1.3/), Tachnical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gromlinl.zcol.iastate.edu/cgi-bin/sp.cgi), Gense mocding trRNAs are predicted by trNAscan-SE (Sean Eddy, Washington University, School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K15E6 and the 3' clone is K3K3.
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Submitted (18-AUG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/KaosoGgi-bin/agd_graph.cgi?c=mxFl2
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'
protein similarity are described as 'unknown protein'
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1PVQTVLNTFFPSLDSLEFVKNIEIFVSLOSLERA
AFBYFXRLNYGGKTVGGSSOFRRWUSDDEIILSESSGTSPIVPDIKINYTEKPPSYVA
PDDVYATSRSMGADHPEQNLNFNLTWLFTVDAGFSYLVRHFCETLSEVNKEGGRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Braßsicaceae; Arabidopsis.
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vsGrnwtaenQrilsSnlvnasFtaQasyQesGVSQIPYWTarifrsEFTySFPvTpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Sato,S., Kaneko,T., Nakamura,Y., Kotani,H., Miyajima,N.
                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana (strain:Columbia) DNA, clone_lib:Mitsui P1
clone:MXF12.
                                                                                                                                                    ABU16892 66237 bp DNA PLN 27-DEC-2000 Arabidopsis thallana genomic DNA, chromosome 5, Pl clone:MXF12. AB016892 BA000015 AB016892.1 GI:3449127
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2613. 5234
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Asamizu, E.,
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ARLRKDLFRHLMHQEIAFYDVTKTGELLSRLSEDTQIIKNAATTNLSEALRNVTTALI
GVGFWTFSSKKLTLLALVVPVISVAVKYGFGRTLRELSHTTQAAAVASIAEBESFGA
GVGFWTFSFAKESYKUJGYSKKVDETIKLGLKQAVLVGLFFGGINAFTLSVITVVSYGA
YLTIYGSMTVGALTSFILYSLTVGSSVSSLSSLYTTAMKAAGASRRVFQILDRVSSNS
                                                                                                                                                                                                                                                                                                                                                                                  SSGDKCPVGNPDGDVELNDVWFAYPSRPSHMILKGISLRLTPGSKVALVGPSGGGKTT
THALERFYDPLKGKILLNOVSLMEISHQYLHKGISIVSOGBPTLENCSYBENIAYGFD
GEASFTDIENAAKMANAHEFIEAFPDKYNTVVGERGIRLSGGQKQRTAIARALLTNPS
VLLLDEATSALDAESSEYLVQDAMDSLMAGRTVLVIAHRLSTVKTADCVAVISDGEVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="Myneemesslkyidvarytpsnsdssesltlpltffbllwyklh
avervifykltdasrpffdsvivpnlktslssslshylplagklywepldprpkivyt
pndavsftvaesnadfsrltgkepfpttelyplypelhysddsasavsfqytlfpnqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCISVNAHHAVLDGKTTTNFLKSWARTCKNQDSFLPQDLIPVYDRTVIKDPMDLDTKI
LNAWHRVAKVFTGGKEPENPKSLKLLMSPEIGPDVFRYTLNLTREDIQKLRERLKKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MVSSLNIIEVARVTPSNSDSAESLSLPLTYFDLIYYKLRAVERV
SFYRTIWTFFDSYLVPNLKTSLSSCLSHYLLPLAGKLIWBPLDHKPTYYSQNDDV
SFYRTIMPFFSPSYLVPNLKTSLSSCLSHYLLPLAGKLIWBPLDHKPTYYSQNDDV
SFYAETNADFSSLSGNEPFPSTELYPLYPALOSSDDSASIYSFOYTLFPNGGECIGY
SAHHAVLOGKTTTMEKSWAHICKHQDFSLPQDLIPTYDRTVIKSPTDSENKVLNEWR
                                                                                                                                                              LEHGVVEAANVGFGRVFALICQYSSIMVSQAKPDAGKLVIGTIALLIGSTTNLLVPKF
GGMIIDIVSRDVKTPEQQTESLIAVRNAVVIILLIVVIGSICTALRAWLFNSASERVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYFETFMSEEGFLAAARMVSDSVEALDENVALKIPEILEGFTTLSPGTQVLSVAGSTR
FGVYGLDFGWGRPEKVVVVSIDQGEAISFAESRDGSGGVELGFSLKKHEMDVLVDLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFTKILAGGKEPANPKSLKLNPSFEIGPDVVRYTLQLTREDIQTLRERLKREVSSSS
STSSSKELRLSTFVIVYSYVLVCIIRARGGEPHRPVGYAFSVDCRSLMNPPTPNYFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIAGCSRWMLTAKWFWGEEGLLAAATWYSDSIEBWDESFAWKIPDFYAYATLPPFTQL
ILVSGSNRFGYYELDFCWGRPDKVMVYSISPGNGISMAESRDQNGSVEIGFSLKKHEM
DTLIDLLHCELTI"
34363. .35709
                                                                                                                                /translation="mGNKKLLTGGSSKTHGSGSSYRDPLLQNQEDKPKANGSENGLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSSVSSPKELRLSTFVIVYSYALTCLIKARGGDPSRPVGYGFAVDCRSLMVPPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCGTCGCCTCACTCTCCCGCTCACTTTCTTTGACCTTCTCGCCTCAAACACAAA 34478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 CCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAAC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 CACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
product="anthocyanin acyltransferase-like protein"
/protein.id="anth010829.1"
/db_xref="G1:10177550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
product="anthocyanin acyltransferase-like protein"
/protein id="gAB10830.1"
/db_xref="GI:10177551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"transposase-like protein" complement(join(30804, 30874,30947, .31289)) /note-"contains similarity to Ac-like transposase gene_dimXF12.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 66237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(27466. .27879,28046. .29073))
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Pred. No. 9.9e-12;
); Mismatches 716; Indels
/product="ABC transporter-like protein"
/protein_id="BAB10828.1"
/db_xref="G1:10177549"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGTHDELLSLNGIYTNLVKRQLQSSSSVTTL"
join(25348. 26359,26401. 26756)
/note="gene_id:MXF12.7"
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/note="gene_id:MXF12.10"
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Matches 664;
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LRLYFYPTQYKSGFDAVNSFFSEAS QCAGGES PYMEARIFREEFYSEPYFESTE
LRLYFYPTQYKSGFDAVNSFFSVKVNGFTLLRNFNADSTVQASIPLSNSLIKEFIIPV
HYTLALTFFFBKNLLAFVNGIEIVSMPDRFYSRGFDNVLRNYSDVDFQIDNSTAFE
SVQTLALTFFFBKNLLAFNTGHELTTVDAGYRYTVRTKLHFCFTLPQVTKRAGORVFSIFVDD
VXATSRLMGNSSNLAFNLTGHELTVDAGYRYTVRTKLHFCFTLPQVTKAGORVFSIFVDD
KMAKKETDVIRLSGGPRIPMYLDFSVYVGFESGMIQPELRLDLVPLKDTNQTYYDAIL
                                                                                                                                                                                                                                   VVKGTFGYLDPEYYRQVLTEKSDVYSFGVVLLEVLCCRPIRMOSVPPEQADLIRMYK
SNYRRGTVDQIIDSDLSADITSTSLEKFCEIAVRCVQDRGMERPPMNDVVWALEFALQ
LHETAKKKNDNVESLDLMPSGEVGTTTDGEDDLFSRTTGHVGKSTTTDDSVLVVGDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MINLEKEAKEKQILIRDGKRKIVHHVNTTLLVKIYEASAIDDRH
LFLKPYYGPPNYYFIKAWLDDTKEYGTYVVKDSFKVNQPPLKIPLLVFPAQYLYVELLK
GMSYRDPGTSNRTVVMGRAKIRLSPLMTSYKERPISGGIDLVGLNSDQCVVKKGYLTY
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LATFIVIIMLLIRQMKRKKNKKENSVIMFKLLLKQXIYAELKKITKSFSHTVGKGGFG
TVYRGNLSNGRTVAVKVLKDLKGNGDDFINEVTSMSQTSHVNIVSLLGFCYEGSKRAI
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KMILVSLWCIRPCPSDRPPMNKVVEMIEGSLDALELPPKPSRHISTELVLESSSLSDG
QEAEKQTQTLDSTII"
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NGVEILKLNNSGNLAIIQDNELKPNPPLSSNLTPNHVTQQIKGKSSHLLVKIFIAVGP
GTGLATFVVVLMLWMRQMKRKNRKEERVVMFKKLLNMYTYAELKKITKSFSYIIGKGG
                                                                                                                                                              LSKLRHVHLVSLIGYCDEDNEMVLVYEYMPHGTLKDHLFRRDKTSDPPLSWKRRLEIC
IGAARGLQYLHTGAKYTIIHRDIKTTNILLDENFVTKVSDFGLSRVGPTSASQTHVST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEFLEHGSLDQFISRNKSLTPNVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKPQN
ILLDDNFCPKVADFGLAKLCEKRESILSLIDTRGTIGYIAPEVVSRMYGGISHKSDVY
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WTQEEKNILPKNSDNASFSSVVSYKEESGIPQVPYMTARIFRSDFTYSFPVSPGWKFL
RLYFYPTSYKSGFDAVNSFVSVTVNDFTLLQNFSADLTVKASIPESKSLIKEFIVPVY
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VYSTCRMMGNAQDTYLNLNFNLTWLFTVDAGFSYLVRLHFFEKYLNKANQRVFSIFLG
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AIVYEFLENGSLDQFMSRNKSLTQDVTTLYGIALGIARGLEYLHYGCKTRIVHFDIKP
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VYSFGMLVIDMIGARSKEIVETVDSAASSTYFPDWIYKDLEDGEQTWIFGDEITKEEK
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                                                                                          SLVVLAMFVVGVLVIMKKKKKKKSKPSTNSSWCPLPHGTDSTNTKPAKSLPADLCRRFSI
                                                                                                                                'EIKSATNDFEDKLIIGVGGFGSVYKGQIDGGATLVAVKRLEITSNQGAKEFETELEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNCNVLFLLSVLVSVTAGVTAAYHPTDVFLFNCGDTSNNVDNSG
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17737. 17461,17541. 17640,17803. 17974,18073. 189191,
18285. 18395,18488. 18652,18712. 18844,18934. 19009,
19232. 19227,19385. 19492,19591. 19698,19873. 20070,
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/product_rereptor protein kinase-like protein"
/protein.id="BAB10827.1"
/db_xref="GI:10177548"
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/protein_id="BAB10826.1"
/db_xref="G1:10177547"
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/protein_id="BAB10825.1"
/db_xref="G1:10177546"
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/evidence=not_experimental
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/note="gene_id:MXF12.4"
/codon_start=1
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/note="gene_id:MXF12.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="gene_id:MXF12.3
                                                                                                                                                                                                                                                                                                                                                SGSSWGVFSEINEPKAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown protein"
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                                                                                                                                                                                                                                                                                                                                CGACTCAGCAGC------AGTCGTGTCGTTTCAAGTCACGTTATTTCCAAA 34820
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AC002560 101176 bp DNA PLN 19-JUL-2000
Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Masnsicales; Barssicaceae; Arabidopsis.
1 (bases 1 to 101176)
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Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kin, C., Altafi, H., Bell, B., Chin, C., Chiou, J., Choi, E., Conn, L., Connard, Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, A., Liu, S., Mukharsky, M., Nuyyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Direct Submission
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Submitted (13-NOV-1997) Arabidopsis thaliana Genome Center,
Department of Blology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
4 (bases 1 to 101176)
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                                                                                                                                                                                                                                    35706 ATGATAATGGAACAAAATRAAGATTTAATTCAGTGTGTCTCTCTTGTTAGCTTGCATCGA 35765
--AGAGAGGAAAGATATCAATTGCGGAGAGTAGAGATGGAAGTGGAGGTGTTGAGATTGG 35645
                                                                                                                                                                          GGGTTGATTAATCATTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTC 1409
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Ecker, J.R.
Direct Submission
                                                                                                                   ATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAA
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Ecker, J.R.
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KWTRLNPIGDVPSPRACHAAALYGTLILIQGGIGPSGPSDGDVYMLDMTNNKWIKFLV
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YCVDALTLENKFSVLIYPYPROPOPVRQGTTRVNVGYGPMAVGPRMLAYASKSSMTMKTGR
LSPOTFFTSSPELLSPSSSSGGSSFMARYAMESSKOLANGLINGDMGYKTLSKYCODML
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SGTLLVTASVCGNNINNFQIMPSKSHNAPGDBSVEMESSHVHLFKLHRGITSALVQDI
CFSQQSQWVALISSKGTCHIFVLNSSGSDAAFQPCEGEEFTRLPASSLPWWFTQSLSS
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PPWWKYPHREYLDTERENSWLTNSLWDTKPLQKCYRISKEFQCRVKSTAQGEDPTLVCS
TPBWAAHIWRSWVKALDVKPLDYNLTFFSVWYRTRLEFTKLRKGFYGNVCLACAM
SSVESLINDSLSKTTRLVQDARLRVSEDYLASMVDVDVRRFKRLEFGGKLTTTGWFR
FEMYETADFGWGKPVYAGPIDLRPTPQVCVLLPQGGVESGNDQSMVVCLCLPPTAVHT
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DQDANSTNALLBULTVSTPSGHVOHELLPSVTESPENGLKTVGKTSHVQVQEDDLRV
KVEDIQWMVCRRSDMLETERELPKSITEKOTETVSNHLTSHEDACLSLDNNSHFS
EDKYLKSCSEKPPERSHCYLSNFEVKVTSGMLPVWQNSKISFHVMDSPRDSSSTGGEF
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/db_xref="G1:9280672"
/translation="MASCIQELHFTHLHIPVTINQOFLVHPSSPTPANOSPHHSLYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIEKVPAHELEIKOKKLLPVFDHFHSTKATLEDRFSMKCYHTSATGSHQVNGKICQDI
INCHSKPGSIESAESSEEGSTKQMENLHDSDHMSNSIKSSLPLYPTVNGIYKEIEKNN
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KAVADPKEEHLKKKLDEVTNVHHLNVNNNNTEKLQGDKMVNSQVLNAFGVCILYKDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLDDI IGARVFTPSVYFYPSTNNRESFVLKRLQDALSEVLVPYYPLSGRLREVENGKL
EVFFGEEGGVLMVSANSSMDLADLGDLTVPNPAWLPLIFRNPGEEAYKILEMPLLIAQ
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gb|T21964.1, and gb|AW004462.1"
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Submitted (15-JUL-2000) Arabidopsis thaliana Genome Center
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complement(4838. .6223)
/note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-not_experimental
/product-"F21B7.1"
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/product="F21B7.3"
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/db_xref="GI:9280639"
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CDS

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                                                                                             37511 CGTCCCGACCCTCCATATTTACACTACAACGCTGGCGAAGACTCTTGTTTTCACCGTA 37570
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                                                                                                                                                                                                                     TACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAA 186
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                                      Gaps
                                                                      7 ACCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTC 66
                                                                                                                                               CCGCTCACCTTCTTCGACATGACGTGCCTGCATTTCCACCCCATGCTTCAGCTTCTTCTTC
                                                                                                                                                                  TCCTTATCTCTAACCCTCAAACACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTA
                                                                                                                                                                                                                                                                                                                            37451 TCCCTCTCCATCACTCTCCAACATTTCTTCCCTTACGCCGGTAAACTGATTATCCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37748 GGCAACTCAGCTACACATGTTGTAGCAGATGGAGTCACCTTCAGTTTCATGAAGTAT
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Length 101176
                                      27;
                   Pred. No. 7.5e-11;
0; Mismatches 718; Indels
DB 12;
Score 102.2;
Pred. No. 7.5
6.7%;
                   Best Local Similarity 45.4 Matches 620; Conservative
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 11914)
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Submitssion
Submited (12-007-1997) Biochemistry, Stanford University/DNA
Sequencing and Technology Center, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, F., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskalar, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submission Submitted (30-JAN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Federspiel, N.A., Palin, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskala, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
38288 GGAGAAAAATGCGTCATGCGTGCTTCAGATGCAATCACAGCGAGAATCAAAGATATTA 38347
                                                                                                                                                                                                                                             38467
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3 (bases 1 to 119314)
3 (bases)
4 to 119314)
Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
Altafi, H., Araujo, S., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Llu, S.,
Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V.,
Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-1999
                                                                                                                                                                                                                                                                                                                             38525 GCATTCTCAGAGTCCAGAGACGCAGCAGTGGAGTTGAGATTGGAATAGCACTAGAGAAG
                                                                                                                                                                                                                      GGATGGGGTAAGGCGGTGNAGCAAGAGATACTGTCGATTGATGGAGAGTTTACGATG
                                                                                                                                                                                                                                                                                                                                                                                                             1246 TCGTTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGTTGGATTGTTTGCCAAAG
                                                                                AGCGACAAGAAGATTCTA3AAACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTG
                                                                                                                                   TCAAGCGATCTGTTGAAGACAGCACCAAGATGGGGACAAGGAGTACGTAAATGGGTCATG
                                                                                                                                                                                      CAAAACTGTTATTTCTCGGTGGGGATCGAGCAGGCTTGATCTTTACGGCGCGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1306 GAGGAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAG 1350
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chromosome I BAC F21M11
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequence.
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SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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AC003027
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COMMENT

FEATURES

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jóin(20752. 20994,21362. 21497,21596. 21740,21825. 21994,
22102. 22178,22542. 22758,22920. 23064,23343. 23442,
23599. 23693,24021. 24072,24227. 24298,24441. 24647)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHTEQDSKRKRDITASDAMENHIKVPKRENNLMQKSADIDCNGKCSANSDDQLSEKIS
KALEQTSSNITICGFCQSARVSEATGEMLY SRGRPVDGDDIFRSNVIHVHSACIEWA
PQVYYEGDYVKNLKAELARGMKIKCYRCSLKGAALGCFVKSCRRSYHPVPCAREISRCR
WDYEDFLLLCPAHSVWFPRSGGFWYSRAPPLPKINPAELCSLEGTPAFTKELVLCG
SALEKSDKKLMESLAYRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKM
IINAAWMKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRVLMGTLRKFF
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ICDEAEEKCSPSTISRKRYPEDSKVKTYEHVYSEESVELSEEKNEEVESEKRSLKSST
TDDQIIEEVASNRSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEETYSDVGFSE
DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGGGVLNPVENLTQWKSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDPQIDDITLSVKPKCRIEPKKLRNQE
LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLNIPRRVTRRDLRPMESVISIYKSLNAAVSVHLPQLQIPNDCNYKNDALNNSNSPKH
GESDOSEMTDKDVSKRSGGTDSSROGSPLPRESEDSPRPKHQWPTEGOLSHLLLLYK
FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNRYTQDP
TLLRLMESLRSDDPTDYVKAQNHQMVYFSFWVIYSFVLCLRSNNLRCVVIFCVQQLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTKLEERDLYFHKLKLTFETALKLRGGPSIVFAHSMGNNVFRYFLEWLRLEIAPKHYL
KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLPVSEGTARLLSNSFASSLWLMPF
SKNCKGDNTFWTHFSGGAAKKDKRVYHCDEEEYQSKYSGWPTNIINIEIPSTSARELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGTLFRAIEDYDDDSKRMLHQLKKYVPFFVIRNIAHRSSLAGFLLYHDDPVFNPLTPW
PRPPTKNVFCIYGAHLKTBVOYYFRDSKRYPDNMITIDLIYFIEGSLVSRSGTVVDG
NAGPITGDETVPYHSLSWCKNWLGPKVNITMAPQILJGKIKQDPEHDGSDVHVELNVD
HEHGSDIIANMTKAPRVKYIIFYEDSESIPGKRTAVWELDKSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement join (16835, 17185,17274, 17392,17491, 17656, 17795, 17885,17982, 18079, 18175, 18361,18504, 18604, 18705, 19049,19134, 19349,19439, 19791,19862, 19967, 20188, 20238), /gene="F2IM114"
//note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AaD10669.1"
/db_xref="G1:4204288"
/translation="MGSSSPEARARAQVPSMILJFLEIICTVHVYTNRRKLNRDVLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDFYKGYKEDLONLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVYNIDPPHGCAL
GEEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
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/db_xref="GI:4204287"
/translation="MGANSKSVTASFTVIAVFFLICGGRTAVEDETEFHGDYSKLSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIPGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKWCVEFGIEANAIVAVPYDWRLS
                                                               complement(join(14567. .14641,14787. .15831,15906. .16006,
16327. .16362))
/gene="F21M11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Unknown protein; Location of ESTs 203124T7, gb|H76794 and 203124XP, gb|AA605510" /codon_start=1
                                                                                                                                                                                    /note="Unknown protein; Location of ESTs 40C3TT, gb|AA728590 and40C3T7, gb|T04573"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REDKSVNWHSTPFEARLEKALNNIDK"
complement(16835, .20238)
/gene="F21M11.4"
               complement(14004. .16362)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD10670.1"
/db_xref="GI:4204289"
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/gene="F21M11.6"
27777. 28734
/gene="F21M11.6"
28007. 28465
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/qene="F21M11.6"
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/gene="F21M11.5"
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       gene
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                                                                                                                                                                        e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', '-ilke' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/section/index.html), GENSCAN (chris Burge,
http://sompio.crnl.gov/section/index.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and
NetPlantGene (S. M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGIKTDLKGYCESWIRINEWINDEWINDEWINDEWINDLKGUEDSSSSUNGIVS
KGIKTDLKGYCESWIRINEWINDEWINGEWINDEWINDLKGYCESWIRINDEWIL
LHFGSWCCSKSKCDGMDAWIFDIDDTLLSTIPPHKRNGFFGGEKLWSTKFEDWIQKK
APAVPHMKKIYHDIRERGIKIFLISSRKEYLRSATVDNLIQAGYYGWSNLMLRGLEDQ
OKEVKQYKSRSKRWLMSLGYRWGYWGDQWSSFAGCPLPRRFFKLPNSIYYYA"
complement(join(14004. .14312,14565. .14641,14787. .15831,
15906. .16006,16327. .16362))
On Dec 30, 1998 this sequence version replaced g1:2734094.
Bassas 1-9262 of clone F21M11 overlap with bases 6898-78259 of
"TAMU" ARC clone F20022 (AC0002411) and bases 119525-119914 of clone
F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="Aad10665.1"
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/db_xref=baparenkkeeekkeeekksrsyatsrgrrkapedyodee
Domdedefplkrrlfsrrgrrsssssssssynnedlktqpeeedddgvtelpplkry
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ECEISGOGMEKAISNMKDITAGEBNVETENWINE INEKVPSKFKWHPHSFYFQDAPVIFS
LSSFSDEGSCSTSCIEDCLASBARGONCAIGVDNGFRYTLDGLLKEEFLEARISEARDO
RKQVLRFCEECPLERAKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRGMHN
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/translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRRNGERGLAMTVYNNASPSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
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WGSEBRLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Proteins in this region are annotated in the F21M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="overlap with bases 68998-78259 of 'IGF' BAC clone F21M11."
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join(13033. .13488,13717. .13926,14139. .14514)
/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(7684. 7866,7965. 8027,8122. 8160,8250. 8381,8458. 8728,8875. 9893,10003. 10256,10344. 10410,10501. 10551,10685. 10781,10885. 10913)
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110C2T7 , gb[f42036, and 110C2XP, gb[A1100245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(13061. ..13488,13717. .13926,14139. .14316)
/gene="F21M11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .119914
/organism="Arabidopsis thaliana"
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1. .9262
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/gene="F21M11.1"
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/gene="F21M11.2"
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E 2 (bases 1 to 85690)

Kaneko,T., Kato,T.. Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission

Lirect Submission

Submitted (b0-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research: 1532-3, Yana,
Kisarazu, Chiba 29:-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-84-85-3935, Fax:81-438-52-3934)

Address for correspondence: Kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi/bin/agd_graph.cgi?c-MOD1
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.
The software progrems used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, hear)

Http://compbio.orml.gov/Grail-1.3/),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thallana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones
DNA Res. 7 (3), 217-221 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
    47094 GGGTCATGTCCCATTATCCAACTCAATTGCAGGAGCTCCGAAATTGGGACTGTATGACA 47153
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACGATGTCGTTGTGTAANCCGAGGGATGCTGCCGGAGGATTGGAGGTTGGATTGTCTT 1297
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Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:MOD1
AB028618 BA000014
                                                                                                                                                           ATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCGGCGGAAATAGAGA
                                                                                                                                                                                                                                                                                             ATATGTTATCAAGCGATCTGTTGAAGACAGCACCAAGATGGGGGACAAGGAGTACGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        47211 GTTCTATCGCATTCTCAGAGTCCAGAGCGCAGCAATGGAGTTGAGATTGGAATAGCAC
                                                                                                               46914 TACCACAAACATACTTTGGCAACTGTATGGCTCCTGGTATCGTATCAGTCAAGAAACACG
                                                                                                                                                                                                     ATTTGCTAGGAGAAAAATGCGTTTTGGCGGCTTCAGATGCAATCACAGGGAGAATCAAAG
                                                                                                                                                                                                                                                      AGAGGACGACCACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGAGATTCGCG
                                                                                                                                                                                                                                                                                                                                         AAGCCTTGCAAAACTGTTATTCTCGGTGGCGGGATCGAGCAGGCTTGATCTTTACGGCG
                                                                     CTCCGGGGAACTACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAGATCCTGCGGCGGG
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/translation-"mntktmrlpprrvltadkrkerdafissytdnppeiakfpsppp
KLVPppvnpiskksstaaaepigsnqlmlagylsheyltqgtlfgeqwnqaraqaess
KIRPSHTVEPAEECEPKRRYREVANLLRSDGAQLPGIVNPAQLARFLKL"
                                                                   complement(29264. .32033)

gene="F21M1.7"

complement(join(29264. .31015,31312. .31414,31484. .31587,

31782. .32033)
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                                                                                                                                                                                  Length 119914;
                                                                                                                                                                              Score 87.8; DB 12;
Pred. No. 7e-08;
0; Mismatches 717;
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|larity 44.9%;
|Conservative |
                                                                                                                                                                                                     Best Local Similarity
Matches 617; Conserv
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47210

FEATURES

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/evidence=not_experimental
/product="Mutator-like transposase-like protein"
/protein_id="BAB02521.1"
/db_xref="G1:119802521.1"
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DTRKDEKRYYQCEKFKDDRTDCMHIRKLWDKAMEEEVSSLRESVDYNRKKVLSHEYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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//db_xref="G1:11994481" |
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ESPML,DDSTFYDALKHIPAELIGENVOTDEVEDEETETNKELACANPVERSAPDDOT
TVIEEEEERSSESDEDVNVEKSVEDEGHEDERDDVIVEKSGEERTIDEDIANVDMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMAMQPLGMYFPVSEYPKKMKLATRCYISEVLKTFADLEHPLTHVEKNYFMEHPSFKH
TATU-BSGYTHKLMRWMLEFRASIERKEWWEVVONPYPIRYCOIREMLAISGENKKAY
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TKTGERASPIDDFCVRSASDLTFCKIFPSGRYSFEYMLKSISHKLDHFNGVVPNTQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPVPGFCVPLEFLAFEAIPSLRERFIEEKEGAHAGCQRWCKVNFKRIEWKGFTLEQIN
HVLGTTEVIESIIREKAEEVPLLAEITGVEDDVDKHDVVVDSWMKRLGQGREIRFEEV
YNEDVQARWEAPNEEEVPTAVGPGDPTLVDVMEKLHSINDKLNEALLVLMEIEEKQAT
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Klsessshdsffstilpklegslalatineiplisghikwdpodpkphyiifpodtys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDGKTASKFYKAWAHICKHGNIPQDFDLPWVLDRTVINVPAGLE
PKLFQLLPYLSKEKVNARNLMLPPAKENINVVRVTLELSEANIKKLKEQAKNESTWSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(33460 .33573,33657. 34016,34094. .34255,
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unknown protein"
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complement(join(42135. .42706,42772. .43162))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strong similarity to unknown protein" /codon_start*1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEMQKELKAHRAEIVNVSKVLFRNPMAPKK"
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similar to unknown protein"
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                                                            /codon_start=1
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29217. .31674
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CDS
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                    (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions.
The 5' clone is T1310 and the 3' clone is T26G12.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MTLHVIETARVTPTDYSVINSANLHKLPLTFFDLPWLLFQPVKR
VFFYELTESTRDHFHSIILPKLKDSLSLILRNYLPLTGHITWEPNEPKPSIIVSENGV
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VAAHHAVLDGKTSSTFIKAWAQICKQELQSMPENLTFSYDRSLIKYPTYLDEKMIELV
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AXAWHCFVKARGGNKDRSVSLLFVOEDRDRLHDPYFRGKUMIPVGCYNRKAAE
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EADFGWGRPVKVDIVSIDQGEAIAMAERRDESGGVEIGMCLKKTEMDSVVSFFNNGLY
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KTESSRDSSTLENLEDGSLSLVLFFLPLSGHLKWNPODKPHYTVFPKDTYSLT
VVESEADFSYISKSELLEFTEPLYPELYPCSSDSSLSLGITLFPNGFFSTGTTVH
HVVWDGKTASKFHKSWAHICKHGTTPQDFDLPTVLDFTVVINVPAGLEQKIFQLSSYIS
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SLKRCEMIVFLSLFSNGFDN"
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YVITCWKRSGGGDANRPVRDNADENRLDDPSPYLTYERONVLLPIDFNGYKATTEL
GKOGYVNGYBILSDSVNGIGSRNIBSIMEVYEDGTKNMKLDYONYTGSNOFGIYGS
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                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mitsui Pl"
2123. .8637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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encoding tRNAs are predicted by tRNAscan-SE
                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                        /strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                  /clone="MOD1"
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Genes
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Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 136047)

Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Ronning,C.M., Koo,H., Fujil,C.Y., Utterback,T., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana 'IGF' BAC 'F7F7' genomic sequence near marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91132 GCGGACACTTTCGTGGAAGGATTTAGTTTTCAGAGTTGGAGTACACAGTTGGGACGATA 91191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91309 GAGTCAGGTGGCGTTGAGATTGGAATGTGTTTGAAAAGACTGAAATGGATTCGGTCGTG 91368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1090 GTGGAGAACTGGCCGTCTGAGATTCGCG----AAGCCTTGCAAAACTGTTATTCTCGGTG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 970 TITGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCA 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1030 GCTGAGGCGATCGCGGCGGAAATAGAGAAGAGGACGAGGACAAGAAGATTCTAGAAACT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1147 GCGGGATCGAGCCGTGATCTTTACGGCGCGGATTTTGGATGGGGTAAGGCGGTGAAG 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 GATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTATCG 969
                                                                                                                                                                                                            Town, C. D. and Kaul, S.

Town, C. D. and Kaul, S.

Town, C. D. and Kaul, S.

Direct Submission

Submitted (01-JUN-2000) The Institute for Genomic Research, 9

Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org

On Jan 19, 2001 this sequence version replaced 91:12280790.

* NOTE: This is a "working draft" sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91012 CCGGTGGGCTGTTATAACCGTAAGGCGGCGGAGTTTATGGAAGAAGGGATTTGTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1267 GCTGCCGGAGGATTGGAGGTEGGATTGTCTTTGCCAAAGGAGAATTGCAAGCTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will
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100213: gap of unknown length
112623: contig of 12410 bp in length
112673: gap of unknown length
116636: contig of 3863 bp in length
116686: gap of unknown length
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Location/Qualifiers
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46028 a 22872 c 22213 g 44783 t
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JOURNAL
                                            REFERENCE
                                                                      AUTHORS
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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*** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16291 GCCGGGTCGACCCGGTTGGGAGTATACGAGGCGGATTTCGGGTGGGGAAGACCCGTTAAA 16350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16231 GCGGACACTTTCGTGGAAGGATTTAGTTTTCAGAGTTGGAGTACACACTTTGGGACGATA 16290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16351 GTTGATATTGTCTCCATTGACCAAGGAGA---AGCGATCGCAATGGCTGAGAGACGTGAT 16407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16468 TCTTTTTTCAACAATGGTTTACATAGCTAAACTCTTGTTTTGTAAGATTTTAATAATAAG 16527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16528 GTAATGCTTGGTTAGTTATTCTTGTTTTTTTCTCACAAGAAGTATTGGGCATAATTCTCC 16587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1030 GCTGAGGCGATCGCGGCGGAAATAGAGAAAGAGGACGAGCACAAGAAGATTCTAGAAACT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1090 GTGGAGAACTGGCCGTCTGAGATTCGCG---AAGCCTTGCAAAACTGTTATTTCTCGGTG 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGGATCGACCAGGCTTGATCTTTACGGCGCGGATTTTGGATGGGGTAAGGCGGTGAAG 1206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1267 GCTGCCGGAGGATTGGAGGTTGGATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGAT 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      970 TITGCGATGCCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCA 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910 GATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCAATCG 969
comptement(46109. .47990)
/note="contains similarity to reverse transcriptase
gene_id:MoD1.13"
                                                                                                                                         /evidence-not_experimental
complement(join(48707, .49066,49148. .49372,49477.
49550. .49982,50772. .51282))
/note-rgpl AAF06688.1
gene_id:WOD1.14
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 85690;
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Arabidopsis thallana chromosome I clone IGF-F7F7,
PROGRESS ***, 4 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 77.8; DB 12;
llarity 48.5%; Pred. No. 7.6e-06;
Conservative 0; Mismatches 287;
                                                                                                                                                                                                                                                                   similar to unknown protein"
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AC069470.10 GI:12320593
HTG: HTGS_PHASE1.
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Patent: WO 0032789-A 40 08-JUN-2000;
AHARONI ASAPH (IL) ; VERHOEVEN HARRIE ADRIANUS (NL) ; LUECKER JOOST
JOHANNES VAN (NL)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAC09066.1"
Aboxete_i01018718185"
//translation="MAAIENYHYEKHEVTKVTPFVNPNSKTTSFTLDLTYFDFFWFK
NPPVERLFFYEMTDLTWDLFNSEILPKLKHSUSFTLLHYLPLAGHIMWPLDAAKPAVY
YFPODNOGYSFAVABWSSECHAGFHHLSGNGIRGAVEHPLYVPOLSLFDDKAPVITY
YTTPPNGGFSIGVSHHAILDGKTSTLFLKSMAYLCKQLOLCHHPCLSPETJPLLDRT
VIKDPTGQOMLQLNKWVGSDNSDPQKIRSLKVLPFLDSESLNKLVRAFFELTREDIT
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1648)
Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLRHKVNHQLSKSSKSKQVRLSTFVLTLAYVFVCMAKAKLAKAKTEAEAAAGNDEIKN
IIVGFTADYRSRLDPPIPLNYFGNCNGRHCETAKASDFVQENGVAFVAEMLSDMVKGI
DADAIEANDDKVSEILEILKEGAMIFSVAGSTQFDVYGSDFGWGRPKKVEIVSIDRTQ
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91369 TCTTTTTCAACAATGGTTTACATAGCTAAACTCTTGTTTTGTAAGATTTTAATAATAAG 91428
                                                          91429 GTAATGCTTGGTTATTCTTGTTTTTTTTCTCACAAGAAGTATTGGGCATAATTCTCC 91488
                                 TITCICGGTGGCGGGATCGAGCAGGCTTGATCTTTACGGCGCGCGATTTTGGATGGGGTAA 1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1257 ACCGAGGGATGCTGCCGGAGGATTGGAGTTGGATTGTCTTTGCCAAAGGAGGAATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71.2; DB 9; Length 1648;
Pred. No. 0.00012;
0; Mismatches 143; Indels 12;
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                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                           AX025514 1648 bp DNA
Sequence 40 from Patent WO0032789.
AX025514
                                                                                                                      /organism="Citrus limon"
/db_xref="taxon:2708"
                                                                                                 1447 TTGAGTCAATAAAAAAAAAAAAAAAAAAA 1475
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/codon_start=1
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Souciet, J.L., Aigle, M., Antiguenave, F., Blandin, G., Bolotin-Eukuhara, M., Bon, B., Brottier, P., Casaregola, S., Ge-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuvedise, C., Ozier Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
1 (bases 1 to 1167)
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TTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAATAATTTTTTTCC 1435
                                                                CNS07360 1167 bp DNA STS 11-JAN-2001 clone BA0AB017A09 of library BA0AB from strain CLIB 210 of Kluyveromyces lactis, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bolotin-Fukuhara, M., Toffano-Nioche, C., Artiguenave, F., Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R., Robert, C., Termier, M., Wincker, P. and Wesolowski-Louvel, M. Genomic Exploration of the Hemiascomycetous Yeasts: 11.
                                                                                                                                         Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="part of mitochondrial DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Kluyveromyces lactis"/strain="CLIB 210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis
FEBS Lett. 487 (1), 66-70 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /variety="lactis"
/db_xref="taxon:28985"
/clone="BA0AB017A09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="BA0AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL427102.1 GI:12210296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyces lactis.
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                                                                                                                                                                                                                                                                                                                                                                                                 CNS07360 1167 bp
clone BA0AB017A09 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kluyveromyces lactis
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/LTAINSTANDING MANANALLEVVQVSPPSSNSITLPLTYFDLGWLKLHPVDRV
LEYHVPELTRSSILSATLHYLPLAGRLWADSIKTKPSIVYSPDDKDAVYL
LPYHPRELTRSSILSATLHYLPLAGRLWADSIKTKPSIVYSPDDKDAVYL
LYAESNVELDSHLSGDEPRPATEFRSLVPELPVSDESARVLAVQVFFPNGFSLGVTA
HHAVLDGKŸTAMELKAWAHKKOGGBALPHDLVPSLDRIIVODPTGLETKLLNRWISA
SNNKPSLKILFPSKIIGSDILRYTRLTREDIKKLRERVETESHAKOLRLSTFVLTYAY
VITCMYKKÄGGDFPRFVCVGFASDFRSKLHPPLPPFFGNCIVGSGDFDVKAPPILEE
GEGKGFTTAVETLTGWVAGLCPENIEKNMLLPFBAFKKMEPGGROMISVAGSTRLGITG
SDFGWGRPVKVETLTGWVAGLCPENIEKNMLLPFBAFKKMEPGGROMISVAGSTRLGITG
JOIN(21572. 21604, 21666. 22065, 22148. 22442, 22710. 22929)
pote="contains similarity to Mutator-like transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mgnlddnkftwviknvptlnsdmlfsnyfviggcswrvvahske

Nnfkseletatijvaedsaqkwcgwsrykiiftlnkoletseretmfdqkssvp

Sethwsigkebhfacfivdelkivvbfeleildklulksenppfkktklnndgev

Skdlirevpvimesivvngffyldsqvefvkrifekhpdvakefrpnrivktaymv

Llslietlrospreisndlogacglirenkakakerprnrivktaymv

Trmreibermkolkakaldvgaplrlddvv"
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WAGELEGGPTEDNEVIYEVDOTVQDPETGSRDDADDDAGDESTVEPPPAYESSQFKKEW
EDSISLTLREEFPSRALHEVVDKGAPRANSGFVIKKSDKERRYNKMHTCTRISKSNT
RMRRRKGTPELVAALLHDTFPGLLETPAPKVIMKLVQTKLGVKISYSTALRGERQAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLKGSAEDSYKDINCYLYMLKKVNEGTVTYLKLDESGKFOYLFTALGASIEGFOAMRK
YLLDATHIKKVSMYSKPHCIRERYNKNSRTYLVPDRSGWDIPDDIKALKVLPL
PRKKKKGRTYVLRFPSTGERRPKROPTONKRLKOCALLFCTHSI"
complement (join (23836. 24188, 24334. 24547, 24687. 24774,
                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
complement(join(10964. .11326,11419. .11702,11802. .11968,
12054. .112160)
/note-"emb[CA868159.1
gene_id:MT024.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translati.on-"MVEERTKILSRKNEKDQAEPASTDPAGWSGQLTLELVDYGSSRV
                                                                                      /product="retroelement pol polyprotein-like" complement(join(9270. .9952,10067. .10153)) /note="contains similarity to copia-like retroelement pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="anthocyanin 5-aromatic acyltransferase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strong similarity to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to unknown protein" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to unknown protein"
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/protein_id="BAB01192.1"
/db_xref="G1:11994163"
                                                                    /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/protein_id="BAB01190.1"
/db_xref="G1:11994161"
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/protein_id="BAB01193.1"
/db_xref="G1:11994164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental complement(15206..16555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="gene_id:MT024.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(12716. .13195)
/note="emb|CAB38296.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAB01191.1"
/db_xref*"GI:11994162"
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/note="emb|CAB61970.1
                                                                                                                                                                                                                gene_id:MTO24.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene_id:MTO24.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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         /codon_start-1
                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                    polyprotein
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Address for correspondence: Kaosékazusa.or.jp

For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?~MTO24

Genes with similarity to proceins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein.'

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail.1.3/), GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and splicePredictor (Volker Brendel, Stanford University, http://gremlini.zool.lastate.edu/cgi-bin/sp.cgi)

Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/cddy/tRNAscan-SE).
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                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S. Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 82360)
Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP000606 82360 bp DNA PLN 27-DEC-2000 Arabidopsis thallana genomic DNA, chromosome 3, Pl clone: MTO24.
                                                                                                                                                                                                             1356 ATTAATCATTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTGTTTGT 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                  clone is T13J10.
                                  57;
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      No. 0.00018
                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and BAC clones
DNA Res. 7 (3), 217-221 (2000)
20363099
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54.5%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP000606 BA000014
AP000606.1 GI:6045161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone:MTO24.
Arabidopsis thaliana
                                  91; Conservative
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
ACCESSION
VERSION
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AP000606/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
REFERENCE
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CDS

CDS

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.49959,50068. .50400,50660. .50698,
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FCRNFQWGRYFFDYMLGTISHTVNHRNGSVTNHRKYVWSVLGFCLPWELLAFEAIPQL
RETFMEDIAGADEGCPRACVRFKKHNHRGFPLDTTYAELGTTGRRERSELIRFDEIY
QQDIQALQITAGPKIAGAEDIPAVGQELFSLVSVVEMIENLDKKWVDQLNEITTMIS
DLDKRVESLEAFKDEQKAEERKNQEEMDGEKDGPIEKDGVQEKDGDGEDGVPKEKD
OEKDGYPKEKDPKEKENDFKEKDGFSKPVENNFTRRITRFFKN"
join(399) .33608,33762. 33830,34025. 34098)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                       /translation-*MDRLCESDPWYDEMKSAKRIMQQLEEVAMMEEIPIICPCGGRIL
DIISEKDGDKGKRYYECTDYKNDGLHIQKLMDKAMVEEVNRLREQVDNHHQKIQSLEY
SNQEVLSEFDEIQKKMGTLMRVRNYWVCYYRYQVFHCILSIPLYSQFSLVFSVLSLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence-int_experimental
//protein_id="BAB01195.1"
//db_xref="G1:11994166"
/translation="MAPRTIPPLKRRRGVAGGTKPIDVVTKATTEPPTTTEEPSATE
ONVALEGOVEEPIPPIIPTVVEEPESDSDNNERESDESEEBEREEE
ENEBEREEGONVGEESSENDSSTTLGEEYSSDKNMDETAYENQVEIPASMIIDEET
KAILPLSMYFPPSEYVKKIKLSIRCYTHEVLTTFDKLEPEMSKSEREWPONHOSFQHI
                                 ELMRMLPPGPTVRWSVEDGEDRSSDGMDREKCSRKHKDKCIRTHPRIAHGCNLTGKGR
KHQEWVRNVIHHIGSISRLPSCIYLLSHGETDRRSVRPNGDSMDNQRESPRWEPMDKT
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NEEGFRSILHVESNMRMNENBRFDKILREDLVRQNVVNNEDTSLIVGTDEIGGAVLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGKREAANDIRGTPEEGFRFVDYYMYMLQKMNHESGSYVEVDEENKFNYLFFALGSSI
EGFRLMRKVIILDGTHMKTAYGGILIVATTQDPVHSRCASPWECARAYTEAEFLRCYF
GGEKYNRDTSNSVESVNGVLEKVRNYSLLQLIDAIVGKIAEWFAKHRKSLELIPSGQY
KRCLGQKHPFAPYIREDAQGLWDHLTTSRHHKTFLKVSQHISKLLVGKGVRLGEYNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVGEPSEVVVENKDIYLEENICGGMSKPYSIRKDSFMISVKYNYRAKFRVQVSYSTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(26878, .27120,27210, .27491,27693, .27854,
27950, .28175,28419, .28702,29026, .29487))
/note="emb|CAB77996.1
                                                                                                                  join(25891. .26085, 26155. .26349, 26412. .26534)
/note="contains similarity to Mutator-like transposase gene_id:MT024.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
join(49318. 49683,49880. 49959,50068. .50400,50660. .
50779. .50980)
/note="contains similarity to Mutator-like transposase
gene_id:MT024.13"
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join(34168. 34242,34530. 35934,36128. 39479)
/note="gene_id:MTO24.11"
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/note="gene_id:MTO24.14
unknown protein"
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/protein_id="BAB01196.1"
/db_xref="G1:11994167"
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/protein_id="BAB01194.1"
/db_xref="G1:11994165"
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                                                 1139 TCTCGGTGGCGGGATCGAGCAGCCTTGATCTTTACGCCGCGGATTTTGGATGGGGTAAGG 1198
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 Length 82360;
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Score 69.6; DB 13;
Pred. No. 0.00037;
0; Mismatches 164;
  4.6%;
                          Conservative
              Similarity
             Best Local Sim
Matches 181;
   Query Match
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	16 80.2 5.3 936 22 AAF58262 Oligonucleotide 17 80.2 5.3 938 22 AAF58255 Oligonucleotide	73.2 4.8 244 22 AAFF30238 71.2 4.7 1648 21 AACF3127 65 4.3 1240 21 AACS3227	22 62.4 4.1 49999 20 23 61.6 4.0 1379 21 24 55.4 3.6 49999 20 25 55 3.6 2418 13	54.6 3.6 3030 21 AAC61886 54.2 3.6 1520 21 AAF15829 54 3.5 2662 10 AAN90703	52.6 3.5 1875 18 AAT48669 51.8 3.4 1213 21 AAC51043 51.9 3.4 1213 21 AAC51043	51.8 3.4 121/ 21 AAC42550 51.4 3.4 318 12 AA010712	5.1 3.4 83.5 20 AAAZAUDS 50.8 3.3 1052 10 AAN30224 50.3.3 1518 17 AAN37313	50 3.3 5173 18 49.8 3.3 1132 20 49.8 3.3 2229 21 49.6 3.3 3138 12	49 3.2 2564 22 AASO0034 49 3.2 4590 7 AAN60472 48.8 3.2 2418 13 AAQ27886	48.4 3.2 1493 11 48.4 3.2 1493 11 48.4 3.2 1493 20	SIN	RESULT 1 AAT37313 ID AAT37313 standard; CDNA to mRNA; 1518 BP.	XX AC AAT37313;	DT 06-FEB-1997 (first entry)	AA DE Aromatic acyl transferase coding sequence.	XA Aromatic acyl transferase; transformation; anthocyanin pigment; XW plants; acylation; colour; tone; colouration; colour change; XW Gentiana trififora; Petunia hybrida; Petilia ocimoides; XW Gentiana trifitana; Achandala annustifolia; Ac	Lavandula angustifolia (Clc	Key		WO9625500-A1.		XX PF 16-FEB-1996; 96WO-JP00348.	64.0	(SUNR) SUNTORY	•
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: November 5, 2001, 18:11:58; Search time 445.49 Seconds (without alignments) 2145.203 Million cell updates/sec	ՐՐՐՐՐՐՐՐՐՐՐՐՐՐՐՐ	Scoring table: IDENTITY_NUC Gapext 1.0	Searched: 730101 seqs, 313950809 residues	Total number of hits satisfying chosen parameters: 1460202	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Geneseq_0601:* /SIDS1/gcgdata/geneseq/geneseqn/NA19	<pre>// ></pre>	5: /SIDSJ/gcgdata/geneseqn/qeneseqn/NN1984.DAT:* 6: /SIDSJ/gcgdata/geneseq/geneseqn/NA1985.DAT:* 7: /SIDSJ/gcgdata/geneseq/geneseqn/NA1986.DAT:* 8: /SIDSJ/gcgdata/geneseq/geneseqn/NA1987.DAT:*	/SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT	13: /SIDSI/gcdata/geneseq/geneseqn/Nal992.UAT:* 14: /SIDSI/gcdata/geneseq/geneseqn/Nal993.DAT:*	10: /siDsilygdata/geneseq/yeneseqn/Nala94.uki:* 16: /siDsilygdata/geneseq/geneseqn/Nala95.Dai:* 17: /singl/nondata/conconconconconconconconconconconconconc	1: /SIDSI/gcgdata/geneseq/yeneseqn/Nal990.UAI:* 18: /SIDSI/gcgdata/geneseq/geneseqn/Nal997.DAI:* 10: /SIDSI/gcgdata/geneseq/geneseqn/Nal997.DAI:*	19: / SIDSI/gegdata/geneseq/geneseqn/NR1999.DAT: 20: /SIDSI/gegdata/geneseq/geneseqn/NR1999.DAT: * 21: /SIDSI/gegdata/geneseq/geneseqn/NR2000.DAT: * 22: /SIDSI/gegdata/geneseq/geneseqn/NR2001.DAT: * 22: /SIDSI/gegdata/geneseq/geneseqn/NR2001.DAT: *	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	% & Query	ore Match Length DB ID Descripti	1505 98.9 1518 17 AAT37313 765.4 50.3 1479 17 AAT37311	196.2 12.9 1/03 1/ AAT3/308 Aromatic 174.2 11.4 1508 17 AAT37312 Aromatic 153 8 10 1 1523 17 AAT37300 Aromatic	6 87 5.7 936 22 AAF58254 Oligonuc	8/ 5./ 536 22 AAF58259/ 87 5.7 936 22 AAF58259 87 5.7 936 22 AAF58262	11 87 5.7 938 22 AAF58255 Oligonucleotide

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Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;

Nakao M, Tanaka Y, Yonekura K;

XX

WHI: 1996-393401/39.

XX

WPI: 1996-393401/39.

XX

DNA coding for aromatic acyl transferase - for transforming plants
PT which produce anthocyanin pigments and thus altering colour tone,
PT e.g. of flowers

XX

XX

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Vectors containing DNA fragments encoding proteins of plant origin
CC with aromatic acyl transferase activity may be used to transform
plants which produce anthocyanin pigments. The aromatic acyl
CC transferase acylates the pigments in the flower resulting in colour
CC transferase acylates the pigments in the flower resulting in colour
CC specific DNA sequences encoding aromatic acyl transferase from
CC different plants are described in AAT37308-T37313. NOTE: This
Sequence is supposed to cross reference with the protein described
CC in AAM04727, however there are so many discrepancies between the
CC polypeptide decoded from this sequence and the polypeptide given in
CC the specification and described in AAW04727 that the indexer decided
XX

Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
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                 Gaps
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                                                                                                                                                                                                                                                                                                                                                     Length 1518;
                Indels
98.9%; Score 1505; DB 17; 99.8%; Pred. No. 1.2e-278;
                ;
               0; Mismatches
        Best Local Similarity 99.8
Matches 1518; Conservative
Query Match
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                         CTACCTACCTTTTCACCCCAATCTGAAATTAAGAAATTGAAGGGTTTGATTCAGAGAAAG
                                                            CCCCAAATGTAGTTAATCTCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCGGCA
                                                                                               GTCTATCGTTTGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGT
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                                                                                                                                                                                                                                                                                                      plants
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Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentlana triflora; Petunia hybrida; Perilla ocimoides;
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                                                                                                                                                                                                                                                                                                   coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour of flowers
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                                                                                                  Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 765.4; DB 17;
Pred. No. 1.6e-137;
1; Mismatches 417;
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                              Lavandula angustifolia; ds
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                                                                   Location/Qualifiers
                                                 ocimoides (Clone pSAT208)
                                                                                                                                                                                                                                         ', Fujiwara H, Fukui
Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
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Best Local Similarity 71.1%;
Matches 1056; Conservative
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P-PSDB; AAW04725.
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                              Scenecio cruentus;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1479
                                                                                                                                                                             30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
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aagatgcagtcccttctcttttacgactttccgtacccaagaacacatttcttggacact 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                      Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides;
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                 Mizutani
       Sequence 1703 BP; 512 A; 353 C; 356 G; 482 T; 0 other;
                                                                                                                                                                                                                                              /*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants are described in AAT37308-T37313
                                                                                                                                                                                                                                                                                                                                                                                               Kusumi T,
                                                                                                                                                                                   Scenecio cruentus; Lavandula angustifolia; ds
                                                                                                                                                                                                       Gentiana triflora var. japonica (Clone pGAT4)
                                                                                                                                     Aromatic acyl transferase coding sequence.
                                                                            ВP
                                                                         AAT37308 standard; cDNA to mRNA; 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 53-57; 94pp; Japanese.
                                                                                                                                                                                                                           Location/Qualifiers
6..1415
                                                                                                                                                                                                                                                                                                                                                                                            Ashikari T, Fujiwara H, Fukui Y,
Nakao M, Tanaka Y, Yonekura K;
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95JP-0067159.
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29-JUN-1995;
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TITGCGATGGCGAAGATCCTGCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCA 1029 GCTGAGGCGATCGCGGCGGAAATAGAGAAGAGGACG----AGCGACAAGAAGATTCTAGAA 1086 gttgcagctattggagaagccattgaaaagaggttgcacaacgaaaaaggcgttcttgca 1142 1143 gatgcaaaaacttggttatcggaatctaatggaatcccttcaaaaaagatttctcgggatt 1202 GCGGGATCGAGCTAGATCTTTACGGCGCGGATTTTGGATGGGGTAAGGCGGTGAAG 1206 636 ggaaatttgttgatgccgatcaaatcgggcgaaatgccgaagtttcagtactcccgtgat 308 ggtcatcaactggtagattccaatgatttgcatggccttttttatgttatgccacgggtt 428 ATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTT 456 ataaaggaccatgcaagactataaagtgatcccgctcgtagccgtgcaagtaaccgttttt 488 CCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACACCCGTTAGCGGATGCTCCATCG 516 ATTAAGAAATTGAAG-----GGTTTGATTCAGAGAAAAGCCCCAAATGTAGTTAATCTC 801 atccagaagctaaagaacaaagtactgaatctcagaggatccgaaccgacaatacgtgta 842 gttatccctaatcttaagccctctttgtctctcactctaaaacactaccttccgcttagc AACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGA---TCATCCGCATTCC GCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCG cctaaccgtggcatagccgtggctctgacggcacatcattcaattgcagatgctaaaagt TITGIAGGGITITATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGAATTC TTGGACGGAAAAGGTGAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCT ttgtccgcga----atcttcttccatctttcgatagatcgataatcaaagatctgtat 637 AAATTGGACACATATTTATGGAACAACGCGCAGAAACGTC-----CGTTGGAATCG TGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAGTTCCGGTA-----TCAG gagggcgactcgataactttgatcgttgcggagtctgaccaggattttgactaccttaaa TCTTCCTTCGTCGCGATCGCAGCTTATATCTGGACCGGCATCGCCAAATC----gtcgtatcagaggaatcatcgaacgacgaaatgagctcgagtacttcagttttacagcg GATTTAAGGCCGCGTTTGGATCCGCCGGCTCCGGGGAACTACTTCGGAAACTGTCTATCG ACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTG 1.083 1147 Db δ g ŏ g ζ

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603; Indels

12.9%; Score 196.2; DB 1751.3%; Pred. No. 6.9e-29; Live 0; Mismatches 603

Conservative

989

Similarity

Query Match Best Local S Matches 686

DB 17; Length 1703;

acagatgtcgagttatcgctaccggtaacattcttcgatatcccctggttgcacttgaat 128 46 ACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCGACATGACGTGGCTGCATTTCCAC 105

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CCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACC 165

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                                                         Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
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tone,
         CAAGAGATACTGTCGATTGATGGAGAAGTTTACGATGTCGTTGTGTAAACCGAGGGAT
                          tttgacattacctctgttgattatgcagaatt---gatttatgtgattcagtccagggat
                                             GCTGCCGGAGGATTGGATTGTCTTTGCCAAAGGAGGAATTGCAAGCTTTTGAT
                                                                                                                                                                                                                                 Aromatic acyl transferase; transformation; anthocyanin pigment; plante; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
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| 3..1867
| 7-tog- a
| /product- Aromatic acyl transferase.
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                                                                                                                                                                                                               Aromatic acyl transferase coding sequence.
                                                                                                                                                      AAT37312 standard; cDNA to mRNA; 1508 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashikari T, Fujiwara H, Fukui
Nakao M, Tanaka Y, Yonekura K;
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95JP-0067159.
95JP-0196915.
                                                                                  1327 GATTATTTGCGGAGGG 1343
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P-PSDB; AAW04726.
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29-JUN-1995;
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DB 17; Length 1508;

Score 174.2; DB 1 Pred. No. 1.1e-24;

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Query Match Best Local Similarity

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TACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAGATCCTGCGGCGGGGATTTGGTCGGA 1008
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                                                                                                       CCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTCTTC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           774 ttaacccaagtgccaaacttggagtacatgtcatcttttacggtaacttgtggttatata
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                                                                                                                                                                                                                                                                                                                                                 ACCCTCCTCGAATCCTCCUGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTC
                                 TACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                              TCGCCGG------AGAAAATGCCGGAGTTCCGGTATCAGAACGGTGACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCATCGGAATAACGACGCACCACACCGTTAGCGATGCTCCATCGTTTGTAGGGTTTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATGTTTGCCGGTTTTCGACCGATCGCTCGTGAATTATCCGCCTAAATTGGACACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggatctccaccggtttttgatagattgatt---aacatcccacatttagatgaaaataag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 tggagttgcatagcgaaatcictcgtaaaaataggagaaaggagggagaagacgagtta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTCGAGGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGAATTCTTGGACGGAAAAGGT
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GACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGAGATTCGCGAAGCCTTGCAA 1128
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                                                                                                                                                                                                    -----ATCATGTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTTGTTTA 1418
                                                                                                                                                                                                                                                                                  1248 ataaatgcaagcaaaacatcagcacaagatcttgaaattggattgagtctaccgagtatg
                                                                                            TGGGGTAAGGCGGTGAAGCAAGAGATACTGTCGATTGATGGAGAGAAGTTTACGATGTCG
                                                                                                                   tgggggaagccgataaagtatgagactgtttcaatagactataatacgt---cgatttct
                                                                                                                                         TTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGATTGTTTTGCCAAAGGAG
                       1074 aataaggacggaatcttgaaagatgccgcgagatggcatgaacctttcatgatcccggct
                                              GAATTGCAAGCTTTTGATGATTATTTTGCGGAGGGAATAAAGGGTTGATTAATCATTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentlana triflora; Petunia hybrida; Perilla ocimoides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag- a
/product- Aromatic acyl transferase.
701..703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scenecio cruentus; Lavandula angustifolia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic acyl transferase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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1322..1324
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/transl_except= AAT e
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95JP-0067159.
95JP-0196915.
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17-FEB-1995;
29-JUN-1995;
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56 atcaaagttcttgagaaatgccgtgttgcgccaccaccggacgccgtcgccgagtttaca 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTACGAACTCCCCTGTTCCAAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTTGCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acaattgcagaatccagcatggattttgattatctcgccggagatcatcagagggattct 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AACGCGCAGAAACGICCGTIGGAAIC-----GCAGCAICCAICITIACCGACG 708
                                                                                                                                                                                                       Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                              plants
tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ACCACCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGACTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGTCGCGGGGGTGTGCATCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gttttggttgacaaatccaatggagattc---attaaagttccttccactttcttctcta
                                                                                                                                                                                                                                                                                                                                                                                             DB 17; Length 1622;
                                                                                                 DNA coding for aromatic acyl transferase - for transforming which produce anthocyanin pigments and thus altering colour e.g. of flowers
               Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                 Mizutani
                                                                                                                                                                                                                                                                                                                                            Sequence 1622 BP; 478 A; 354 C; 313 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 652;
                                                                                                                                                                                                                                                                                                                                                                                           Score 153.8; DB 1 Pred. No. 8.4e-21;
               Kusumi T,
                                                                                                                                                                            Claim 4; Page 57-61; 94pp; Japanese.
             ľ, Fujiwara H, Fukui Y,
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                           10.18;
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                                                             WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                              P-PSDB; AAW04723
             Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                            692;
                                Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
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                                                                                   WPI; 2001-159728/16
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                                                                                                                                     a single surface
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                                                              Umek RM;
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AAF58254/C
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AC AAF582
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DT 24-APR
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                                                                                                                                                                                                                                                                                                                                                           gatgctatccataagaggttacatgactacgaaggaattctgagaggaggtggattggatatcg 1189
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                                                                                                                                                                                                                                                                                   985 ATCCTGCGGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCG 1044
                                                                                                                                                                                    924
             710 gaaagaaaactgctcaaatctcagggcacacctactgttctaaatccagcaatttctaaa 769
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                                                              gatgaagttcgagccaccttcatcctacaccctattgatatcatgaagctcaagaaattc
                                                                                                             atttcgtcaaaaaatcgcaacttaaccggtagtagtaattataatctgtcaactttcacg
                                                                                                                                                   TTGGATCCGCCGCCTCCGGGGAACTACTTCGGAAACTGTCTATCGTTTGCGATGGCGAAG
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                                                                                     ATTCAGAGAAAAGCCCCAAATGTA - - - - - - - - - - GTTAATCTCTTCCTTCGTC
                                                                                                                                    814 GCGATCGCAGCTTATATCTGGACCGGCATCGCCAAAT-----CGGTCGGAGATTAC
                                      GATCGGATTCGAGCTACCTATTTCACCCAATCTGAAATTAAGAAATTGAAGGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                 CCGTCTGAGATTCGCGAAGCCTTGCAAAACT-----GTTATTCTCGGTGGCGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1430 tttacgaatttcatcaatagt 1450
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990 GCGGCGGGATTTGGTCGGAGATGAAGGGGTGTTTCGGGCAGCTGAGGCGATCGCGGGGGA 1049
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                                                                                                                                                                     Nucleic acids containiny electron-transfer group, useful as labels i
hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 5.7%; Score 87; DB 22; Similarity 6.2%; Pred. No. 4.3e-08; 33; Conservative 295; Mismatches 205
                                                                                                                                                                                                                                                                                     Example 6; Page 127; 159pp; English
(CLIN-) CLINICAL MICRO SENSORS
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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Best Local Similarity 6.2%; Pred. No. 4.3e-08;
Matches 33; Conservative 295; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                          Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                            gene expression; ss
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6.2%; Pred. No. 4.3e-08;
tive 295; Mismatches 205; Indels
                                                   ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259.
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Best Local Similarity 6.2%
Matches 33; Conservative
                                                   Electron-transfer group; gene expression; ss.
                 Oligonucleotide D1875
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                                                                                                            Synthetic.
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1050 AATAGAGAAGAGGACGAGCGACAAGAAGATTCTAGAAACTGTGGAGAACTGGCCGTCTGA 1109
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 1170 TTACGGCGCGGATTTTGGATGGGCGTGAAGCCAAGCAAGAGATACTGTCGATTGATGG
                                                                                                                                                                                                                                                                                       group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259.
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1230 AGAGAAGTTTACGATGTCGTTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGTTGG 1289
                                                                                                                                          1350 GGGTTGATTAATCATTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTC 1409
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gene expression; ss.
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17-MAR-2000; 2000US-0190259
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                         The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (FTM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                             Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
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  (CLIN-) CLINICAL MICRO SENSORS INC
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                                                                                                                                                                                                                                                                                                                                   1230 AGAGAAGTTTACGATGTCGTTGTGTAAACCGAGGGATGCTGCCGGAGGATTGGAGGTTGG 1289
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                                                                                                                                                                                                                                                     1110 GATTCGCGAAGCCTTGCAAAACTGTTATTTCTCGGTGGCGGGATCGAGCAGGCTTGATCT
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                                                                                           5.7%; Score 87; DB 22; Length 93 larity 6.2%; Pred. No. 4.3e-08; Conservative 295; Mismatches 205; Indels
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                                                        Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other
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AAF58255 standard; DNA; 938
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17-MAR-2000; 2000US-0190259.
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                                                                                                      Local Similarity
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Matches 33,
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                  ilarity 6.2%; Pred. No. 4.3e-08;
Conservative 295; Mismatches 205;
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4.3e-08;
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                     Best_Local Similarity
Matches 33; Conserv
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                     Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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ilarity 1.3%; Pred. No. 8.6e-07;
Conservative 219; Mismatches 92;
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17-MAR-2000; 2000US-0190259.
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Electron-transfer group; ETM; mismatch; genotyping;
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5.3%; Score 80.2; DB 22
Best Local Similarity 1.3%; Pred. No. 8.6e-07;
Matches 4; Conservative 219; Mismatches 93
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                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC.
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17-MAR-2000; 2000US-0190259
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                                                                                  ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            electron-transfer
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17-MAR-2000; 2000US-0190259
  (first entry)
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                                                                                  Electron-transfer group;
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                                         Oligonucleotide D1954
                                                                                                        gene expression; ss
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             иимимимимимимимимимими сстанимимимимимимимимимимимимими 428
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                                                                                                           mismatch; genotyping;
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5, 2001, 18:12:08

Search completed: November

Job time: 15463 sec

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Patent No. 5198345
Sequence 4, Applination of 198345
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Sequence 1, Appli
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Sequence 18, Appl
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Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-248-35-19
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SPETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                             GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY AGENT: 18-PORMATION:
NAME: BENT, SLEPPEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEFONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 14, Application US/08232463 Patent No. 5670367
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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ADDRESSEE: Foley & L.
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ZIP: 22313-0299
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SEQUENCE CHARACTERISTICS:
                                    nucleic acid
EDNESS: single
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; CLONE: PTZ9Pt-F1s
US-08-232-463-14
                                                                      linear
                                                 STRANDEDNESS:
TOPOLOGY: line
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                                                                 5 CCACCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCAC 64
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3.7%; Score 57; DB 1; Length 7218; larity 4.1%; Pred. No. 0.00037; Conservative 210; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley 6 Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 2213-0229
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DI
SOFTWARE: PAtentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-AUG-1991
AATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
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Query Match
Best Local Similarity
Matches 15; Conserva
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     Length 7218;
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APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
Query Match 3.7%; Score 56.8; DB 1; Length 7
Best Local Similarity 4.0%; Pred. No. 0.00041;
Matches 16; Conservative 225; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1102 RRRRRRRRRRRRRRRRRRRRRRRRAT 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
CURREW APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
PCT-US96-10618-1
PCT-US96-10618-1
Squence 1, Application PC/TUS9610618
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Porter Drive CITY: Palo Alto
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1703 CTTTTAAAAGATTTTGTGTGGTTTTGGTGCAAGTCAGAATAAATTCTGGCTAGTTGAATCC 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Ketth L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
STATE: PA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
RIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORIEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.6; DB 5;
Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.5%; Score 52.6; Di
Best Local Similarity 56.7%; Pred. No. 0.00;
Matches 97; Conservative 0; Mismatches
               APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                           NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/07867106
Patent No. 5389526
                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
MMEDIATE SOURCE:
LIBRARY: Rheumatoid Synovium
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
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COMPUTER: IBM PC COMPALIDLE
CORPETING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
                                                                                                                                                                                                                                                    3.4%; Score 51.4; DB 1;
ilarity 59.1%; Pred. No. 0.0054;
Conservative 0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-789-1400
TELEFAX: 713-789-2679
                        TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
35,134
                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                    LENGTH: 3138 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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LENGTH: 5173 base pairs
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 88; Conserv
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                                                                                                                          TYPE: NUCLEIC STRANDEDNESS:
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                                                                                                                                                                                           ; ANTI-SENSE:
US-07-867-106-4
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1859 AATGGTTTAAAAAAACTTGGGTTGGTTAATTATTATTGAAAATTTTAAAAACCCAAATTA 1918
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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Pred. No. 0.014;
0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/867,106 FILING DATE: 19920625 PRIOR APPLICATION NUMBER: AD PJ 7187 APPLICATION NUMBER: PCT/AU90/00530 FILING DATE: 02-NOV-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  ; Sequence 4, Application US/07867106
; Patent No. 5389526
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; Sequence 2, Application US/07867106
; Setent No. 538926
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.39
Best Local Similarity 65.29
Matches 73; Conservative
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STRANDEDNESS: single
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                                      1514 TTTTTTT 1522
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US-07-867-106-4
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                                                                                                                                                                                                                            4982 AATTTAATGCCAAAGTTTGCCATGTGCCTTAAACATATACTATAATATTTCCCCTTTA 5041
                                                                                                                                                                                                                                                                            1388 AIGAAAICCICIGITICAICTIAITGIIIAAACAAIAAITIIITIICCAIIGAACIIIII 1447
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                                                                                                                                                                      Gaps
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5198145-15
7 PALEDI NO. 5198345
7 PALEDI NO. 5198345
7 DAVID I.; BUXTON, FRANCIS P.; PICKETT, MARK H.;
DAVIES, ROGER W.; SCAZZOCCHIO, CLAUDIO
7 TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNCI
7 NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F198345-15/c
;Patent No. 5198345
; APPLICANT: GWINE, DAVID I.;BUXTON, FRANCIS P.;PICKETT, MARK H.
;DAVIES, ROGER W.;SCAZZOCCHIO, CLAUDIO
; TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNCI
; NUMBER OF SEQUENCES: 28
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                                                                                                                             3.3%; Score 50; DB 1; Length 5173; 56.8%; Pred. No. 0.013;
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                                                                                                                                                                    70; Indels
                                                                                                                                                                                                                                                                                                                                                  1448 TGAGTCAATAAAAAAAAAAAAAAAAAAAAAAAATGAAAAA 1489
                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 49.8; DB 6;
82.6%; Pred. No. 0.0044;
tive 0; Mismatches 12;
                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/811,404
FILING DATE: 20-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/811,404
FILING DATE: 20-DEC-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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Matches 57; Conservative
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Matches 57; Conservative
MOLECULE TYPE: CDNA
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Matches 92; Conserv
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                                ; NAME/KEY:
; LOCATION:
US-08-242-677-1
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                                                                                                                               Query Match
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Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
Sequence 1, Application US/09665309
GENERAL INFORMATION:
APPLICANT:

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TITLE OF INVENTION: Absclatc Acid Responsive Element -Binding Transcription Fac
TITLE OF INVENTION: Absclatc Acid Responsive Element -Binding Transcription Fac
CURRENT APPLICATION NUMBER: US/09/664,800
CURRENT FILING DATE: 2000-09-19
PRIOR PELING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
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                                                                                                                                                                                                                                                                                                                           Length 1578;
                                                                                                                                                                                                                                                                                                                    Score 49.2; DB 4; Length 1 Pred. No. 0.014; 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1448 TGAGTCAATAAAAAAAAAAAAAAAAAAAAAAAAAATGAAAAA 1489
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                                                                FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09664800 Patent No. 6218527 GENERAL INFORMATION: APPLICANT: APPLICANT:
                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-416-050A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thallana
US-09-664-800-1
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 67.6%;
Matches 69; Conservative
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Best Local Similarity
                                                            SOFTWARE: Fast
SEQ ID NO 1
LENGTH: 1578
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LENGTH: 1578
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US-09-416-050A-1
Sequence 1, Application US/09416050A
Factor No. 619459
GENERAL INFORMATION:
APPLICANT: KIM. Soo Young
TITLE OF INVERTION: Absistc Acid Responsive Element -Binding Transcription Factors
FILE REFERENCE: 1942/42
CURRENT APPLICATION UNDER: US/09/416,050A
CURRENT FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 83
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TITLE OF INVENTION: Milliams, Reith L

TITLE OF INVENTION: Improved plasmid Vectors for Cellular

TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz 6 No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STREE: PA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Pred. No. 0.017;
0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFFWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/867,106

FILING DATE: 0920625

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PJ 7187

APPLICATION NUMBER: AU PJ 7187

APPLICATION NUMBER: BCT/AU90/00530

FILING DATE: 02-NOV-1989

ATYONEY/AGENT INPORMATION:

NAME: FEENCE/DOCKET NUMBER: 35,134

RESTERNCE/DOCKET NUMBER: 35,134

RELEPHONE: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: 215-568-3100

TELEFAX: SEO ID NO: 2: SEQUENCE CHARACTERISTICS:

LENGTH: 5852 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

MIDPOLOGY: Innear
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 69.8%
Matches 67; Conservative
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2378..5038
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION:
US-07-867-106-2
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LOCATION:
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1364 TTTAATCATGTATTATGAAGTTGGATGAAATCCTCTGTTTCATCTCTATTGTTTAAACAA 1423
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Best Local Similarity 61.1%; Pred. No. 0.016;
Matches 77; Conservative 0; Mismatches 49;
                                                                                                                         ; Sequence 16, Application US/08330108
; Patent No. 5795752
; GENERAL INFORMATION:
; TILLE OF INVENTION: IL-2-Stimulated Gene
; TILLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 5, 2001, 18:05:10 Job time: 15110 sec
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/104,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: APPLICATION NUMBER: US/07/796,066
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE: T-cell blast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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CITY: Boston
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                                                                                            RESULT 15
US-08-330-108-16
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                                                                                            Gaps
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ROBEY, PAMELA G
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
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                                                     DB 4; Length 1578;
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                                                   Score 49.2; DB 4; Length 1
Pred. No. 0.014;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49.2; DB 4; Length 1
Pred. No. 0.014;
0; Mismatches 33; Indels
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Pred. No. 0.021;
0; Mismatches 41; Indels
                                                                                                                                                                                                  Sequence 1, Application US/09661569
Patent No. 6245905
GENERAL INFORMATION:
TITLE OF INVENTION: Abscistc Acid.Respons:
FILE REFERENCE: 1942.42
CURRENT APPLICATION NUMBER: US/09/661,569
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 09/416,050
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-09-661-569-1
                                                     3.2%;
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Best Local Similarity 64.0%;
Matches 73; Conservative
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Best Local Similarity 67.6%;
Matches 69; Conservative
                                                  Query Match
Best Local Similarity 67.69
Matches 69; Conservative
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5340934-5
;Patent No. 5340934
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US-09-665-309-1
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(without alignments)
2473.399 Million cell updates/sec
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM nucleic - nucleic search, using sw model
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Perfect score:
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em_estrol9:*
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em_estrol.6:*
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em_estrol8:*

em_estrol.5:*

em_estro9:* em_estro10:*

em_estro8:*

9b_est110:*
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em_gss_fun:*
em_gss_hum1:*
em_gss_hum1:*
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565666666666666666666666666666666666666	9b est99; 9b est100; 9b est1100; 9b est1100; 9b est1101; 9b est1105; 9b est1105; 9b est1105; 9b est1105; 9b est1105; 9b est60; 9b est60; 9b est60; 9b est71; 1; 9b est91; em esthum3 em esthum3 em esthum3 em esthum3 em estro21 em estro22 em estro23 em estro23 em estro23 em estro23 em estro23 em estro39; 9b est91; 9b est1107; 9b est1107; 9b est1107; 9b est1109; 9b est1109; 9b est1109;
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em_gss_hum9; *
em_gss_huv1; *
em_gss_lnv1; *
em_gss_lnv2; *
em_gss_pln1; *
em_gss_pln1; *
em_gss_pln1; *
em_gss_pln2; *
em_gss_pln2; *
em_gss_rodd; *
em_gss

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb-gss31:* gb-gss32:* gb-gss34:* em_gss_inv4:* em_gss_rod6:* em_gss_rod7:* em_gss_rod8:* gb-gss35:* gb-gss35:*

TITLE Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Incompatible Reaction JOURNAL Unpublished (2000) COMMENT Contact: Cathy Rouning The Institute for Genomic Research	For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R. FEATURES 1. Gottion/Qualifiers /organism="Solanum tuberosum" /cultivar="Kennebec" /db.xref="Kexon:4113" /clone="HpLI10AA4# /clone="HpLI10AA4# /clone="HpLI10AA4# /clone="lib="P. infestans-challenged leaf" /dov statom="Access colored leaf" /dov statom="Lib="P. infestans-challenged leaf"	/uab_host="SolR" /lab_host="SolR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Xhoi; Whiche plants were challenged with 450,000 short plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Blotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans. US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato." BASE COUNT 212 a 162 c 156 g 233 t	Query Match 10.4%; Score 159; DB 155; Length 763; Best Local Similarity 56.6%; Pred. No. 7.2e-23; natches 314; conservative 0; Mismatches 240; nidels 1; Gaps 1; Qy 25 CGAGTGGCGCGCCCTCCAGGC-ACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTGGA 83 1	Qy 84 CATGACGTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTC 143 Db 64 TCATGTTTGGTTAGGGTTCCACCGTATAGTTATTCTACAGGTCCCCATTC 123 Qy 144 CAAACCGCCTTCCTCGAAACCGTCGTTCCGAAACTCTATCTCTTAACCCT 203 124 CAAACCGCTTCTCTCGAAACCGTTCTCCGAAACTCTCTCT	Qy 264 GGAGTTCCGGTATCAGAACGGTGACTCGGTTCTTTCACGATTATGGAGTCTGTCGGAGA 323 	Qy 324 TCATCCGCATTCCGCTCATAAATACTACTGCCTTGCCCCTAGCGACGATTATGAAGATCT 383 L	Oy 444 AGTGACTCTGTTTCCCGGTCGCGGGGTCTCGGATAACGACGCCCCCCCC
SUMMARIES Result Query No. Score Match Length DB ID Description	159 10.4 763 155 BG591758 157.2 10.3 690 155 BG59447 146.6 9.6 606 113 AW221049 138.8 9.1 570 142 BB922784 138.6 9.1 583 113 AW221050 124.8 8.2 564 142 BB921494 123 8.1 574 142 BB922746 121.8 8.0 687 111 AW102336 119.4 7.8 508 173 BG097054 116 7.6 559 167 BE434557	12 112 7.4 518 119 205.020 AW650280 AW650280 AW650280 AW650280 AR650280 EST328734 13 108 7.1 487 118 AW616206 EST37245 EST37245 15 97.8 6.4 456 142 BE923372 BE9223572 EST4700516 16 97 6.4 436 173 BG097680 BE922378 BE922378 EST472147 18 97 6.4 411 42 BE9221953 BE8221952 EST4756147 18 97 6.4 414 42 BE921953 BE9221952 BE921953 EST4756147 19 95.4 6.3 368 142 BE921953 BE921953 EST475712 20 92 6.0 307 142 BE920010 BE9210953 EST423779 21 86 5.7 408 142 BE920022 BE922095 EST423777 22 86 5.6	84.8 5.6 490 110 AW038515 AW038515 83.2 5.5 409 111 AW033479 AW033479 81.8 5.5 409 111 AW033479 BE920468 BE920468 81.8 5.4 788 164 BE187619 BE187619 79.2 5.2 597 120 AW774948 BF642724 79 5.2 654 151 BF642724 BF642724 79 5.2 657 118 AW692527 AW586972 79 5.2 677 118 AW586972 AW586972 78 5.2 677 118 AW586972 AW586972	77 5.1 311 166 BB353747 76.6 5.0 334 143 BF053201 73.4 4.7 1101 219 CNS00293 71.2 4.7 676 153 BG455847 71.2 4.6 526 166 BB323055 70.4 6 422 155 BG589694 69.8 4.6 649 117 AM560686	ALIGNMENTS RESULT 1	BG591758 LOCUS BG591758 763 bp mRNA EST · 12-APR-2001 LOCUS BG591758 763 bp mRNA EST · 12-APR-2001 DEFINITION EST499600 P. infestans-challenged leaf Solanum tuberosum cDNA clone ACCESSION BG591758 VERSION BG591758 1 GI:13609898 KEYWORDS EST. SOLARED	ORGANISM ORGANISM AUTHORS

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Thu Dec

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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pBlueScript SK(-); Site_1: EcoR1, Site_2: Xho1, cEEF - Fruit were tagged at the lon stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW221049 606 bp mRNA EST 07-DEC-1999
EST297518 tomato fruit mature green, TAMU Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seeds and locules were discarded prior to freezing the
  TTCAATTATCTCATTGGTGACCATCGGCGTAATGCTAAGGATTTTTATCACTTTGTTCT 368
                                                                                                         369 ACGTTAGGGGAACCTAAGGATGCACCCGGGGTCCAATTAGCTCCGGTCTTAGCCATTCAA 428
                                                                                                                                                   GTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACACGGTTAGC 504
                                                                                                                                                                         505 GATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGGGCCTTCCATCACTAAATTCGGAGGA 564
                                                                                                                                                                                                                                                             2 TGACCACCCTCCTCGAATCCTCCCGAGTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGT 61
                                                               385 CAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="tomato fruit mature green, TAMU"
/tissue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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33.4%; Pred. No. 2.6e-20;
tve 0; Mismatches 269; Indels

    606
    /organism="Lycopersicon esculentum"
/cultivar="TA496"

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100 Jordan Hall, Clemson, SC 29634, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clone cLEF3F1, mRNA sequence
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/clone="cLEF3F1"
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Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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Best Local Similarity 53.4%;
Matches 308; Conservative
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JOURNAL
COMMENT
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AUTHORS
                      309
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AW221049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Sateridae; euasteridas; Solanaceae; Solanum.

(bases 1 to 690)

van der Hoeven,R., Bezzeridae,J., Sun,H., Cho,J., Chiemingo,A., Beugli,C., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from sprouting potato eyes unpublished (2000)

Contact: Cathy Ronning

The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
                                                                                                                                                                       EST504342 cSTS Solanum tuberosum cDNA clone cSTS25122 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 AAACACTICITCCCCCTITCAIGCAAICIAATCIACCCICIAICGCCGGAGAAAIGCCG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTC 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 155; Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 157.2; DB 155; Lengtl
Pred. No. 1.7e-22;
0; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="texon:4113"
/clone="cSTS5122"
/clone="cSTS757575"
                                                                                                                                                   mRNA
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55.2%;
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BG599447
                        544 AGATGAACAATTCTT
564 AGATGATGAATTCTT
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KEYWORDS
SOURCE
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Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Llang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in light of trone in the control of trone in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Sukaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae, Solanum;
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AW221050
AW221050.1 GI:6532734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 CGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCATAAATACTACTGCTTTGCCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CACTCCCGCTCACCTTCTTCGACATGACGTGGCTGCATTTCCACCCCATGCTTCAGCTTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 CACTCCCTCTTACTTTTGATCATGTTTGGTTAGGGTTCCACCGTATACGGCGGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AGGATTTTTATCACTTTGTTCCTACGTTAGGGGAACCTAAGGATGCACCGGGGGTCCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 TAACGACGCACCACCACTAGCGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGGG
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                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                               le-18;
hes 252; Indels
                                                                                                                                                                                                                                                                                                      DB 142;
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                   Score 138.8;
Pred. No. 1e-
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136 c 115 g
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                                                                                                                                                                                                                                                                                                                                                                 290; Conservative
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanum.

[ pases 1 to 570)
van der Hoeven, R.S., Bezeridaes, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning
C.M., Fry, M.E., Tanksley, S.D. and Baker, B.
Generation of Essis from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST426553 potato leaves and petioles Solanum tuberosum cDNA clone cSTB22E2 5' sequence, mRNA sequence. BE922784.1 GI:10448860 EST.
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The Institute for Genomic Research
For clone request: please contact Research Genetics,
Division tel 1-800-711-6195, email cdnafresgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_1bb-"potato leaves and petioles"
/clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/dev_stage-"8 weeks old plants"
/lab_host-"SOLR"
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/cultivar="Kennebec"
/db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                        seeds and locules were discarded prior to freezing the
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                                                                                                                                                                                            /db_xref="taxon:4081"
/clone="CLEF3F3"
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/tissue_type="fruit pericarp"
/dev.stage="mature green (3-5 days pre-ripening)"
/lab_host="SOLR"
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                                                                                                                                                                   /organism="Lycopersicon esculentum"/cultivar="TA496"
tomato fruit tissue
           Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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( pases 1 to 564)

van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                             \rm EST425179 potato leaves and petioles Solanum tuberosum cDNA clone cSTB13B18 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTCTTCTACGAACTCCCCTGTTCCAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATGGTTCGGTTTTGGCTATATGCGTCGGATTTTATTCTACAAGCTACCAATTTCCAAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTICITCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATCATCTCATTGGTAACCATCCTCGAAATG---CTAAGGATTTTTATCCCCATTCCTCAA 396
   02-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCCACCTCCCCACGCGCGCGCAACAGAGCTAACGCTCCCTCTAACTTATTTTGATCAT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124.8; DB 142; Lengt
Pred. No. 7.9e-16;
0; Mismatches 242; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib-"potato leaves and petioles"
/tissue_type-"leaflets and petioles"
/tissue_stage-"8 weeks old plants"
/lab_host-"SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB13B18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 t
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564 bp
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                                                                                                                                                                                             potato.
Solanum tuberosum
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4444 Forest Park Farkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Farkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Farkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.edu
Email: est
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Spermatophyta; Maynoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Organism="Glycine max"
/db_xref="taxon.3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1009-1284"
/clone=11b="GGn-c1009"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from entire roots of 2-month-old 'Williams' plants that were greenhouse grown in 5-gallon pots. To suppress nodulation, Black Gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW102336 687 bp mRNA EST 21-NOV-2000 sd86d06.yl Gm-c1009 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1009-1284 5' similar to TR:Q92WB4 Q92WB4 F21M11.13 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                300 TAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTGACATTTTTCC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GAATCTTGGCATATCCGTTGGTTTTAGTAACCATCTCGTGTGTGGAAATACCAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 TCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGAT
                                                                                                                                                                                                                                                                   243 TGGTAACCATCCTCGAAATG---CTAAGGATTTTTATCCCATTCCTCAATTGGCACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 CGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACACCGTTAGCGATGCTCCATCGTT
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                                                                                                                                                                                                                                                                                                                                                                                399 AGTCGAGGAATCTGATCG3AAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCC
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High quality sequence stop: 431.
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For act of Contact: Cathy Rouning

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Location tell 1-800-711-6195, email cdnaéresgen.com.

Location (2000)

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Location/Var-"Kennebec"

About 1-574

About 1-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE922746 574 bp mRNA EST 02-OCT-2000 EST426515 potato leaves and petioles Solanum tuberosum cDNA clone cSTB21L12 5' sequence, mRNA sequence.
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                                                                                                                                                                                                             448 ACTCTGTTTCCCGGTCGCGGGTGTGCGAATAACGACGCACCACACCGTTAGCGAT
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Pred. No. 1.9e-15;
0; Mismatches 215;
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Best Local Similarity 54.9°
Matches 265; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          potato.
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JOURNAL
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           Autripose potening soil was supplemented with: U.Sog/L.

available phosphoric acid (P205), 20mg/L urea N, 0.16g/L.

S, 0.49mg/L B. 2.5mg/L Cu, 0.15g/L Fe, 13.53mg/L Mn,

0.26mg/L Mo, 14mg/L Zu, 20mg/L Ca, and the following
nutrients in a slow-release form (Osmocote): 0.165g/L
ammonia N, 0.185g/L nitrate N, 0.35g/L available
phosphoric acid, and 0.33g/L soluble potash. No nodules
were visible on the roots at harvest. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
CDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated CDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
GGAGAGAGAGAGAGAACTAGTCTCGAG(T)-18]. After
second-strand synthesis primer was used
GGAGAGAGAGAGAGAACTAGTCTCGAG(T)-18]. After
second-strand synthesis primer with Xiol;
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with Xiol;
all XhoI sites in the CDNA would be protected by their
hemimethylated status. The CDNA constructs were
size-fractionated with a 400bp cutoff, using a SizeSep 400
Spun column from Pharmacia. The column eluent was then
ligated into Stratagene's pBluescript II XR Predigested
vector (pBluescript II SK(+) that had been digested with
ECORI and XhoI, and phosphorylated). Both the white and
blue colonias appear to contain recombinant plasmids with
column inserts. This library was constructed by Dr. Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
All-Purpose potting soil was supplemented with: 0.36g/L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 CATACGCTACCTTGATGGAGACTCTCTCTCTTCACCGTTGCAGAGTCCACCGCAGACTT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 CACCCTCCTCACATCAGATTCACCACAAGACGTTCCAAATTGGCACCCTCTTGTTCCCGC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTCCTACCCCACGTGTTGACCAAGATGGCGCACGTGTTCTTTCCTTTATGGCCATTCA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTACAATTTTCCCAAAGTCTGGCTTCACCATATGTCTCACCTTCAACCACCTTGCCAG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 AGTGACTCTGTTTCCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACACCGTTAG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGATGCTCCATCGTTTGTAGGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AGTGGCGCCCCCCCAGGCACGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACAT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 TCATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 121.8; DB 111; Lengt
Pred. No. 3.3e-15;
0; Mismatches 254; Indels
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247 c 91 g 187 t
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Matches 286; Conservative
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                                                                                                                                                             potato.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases I to 508)
van der Hoeven, R. S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Ulterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
                                                          EST461573 potato leaves and petioles Solanum tuberosum cDNA clone cSTB45P9 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGTGGCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCACTCTCAAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCGTTATGTGACTGGAGATTCTATATCTGTTACTTTTATTGAGACTGATATGAATTTC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 AATCATCTCATTGGTAACCATCCTCGAAATGCTAAGGATTTTTATCCCTTCATTCCTCAA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAAA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCGCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACATG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAAATGCCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 119.4; DB 173; Lengt
Pred. No. 1e-14;
0; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 508
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB45P9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164
                                           mRNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

E I (basea I to 659)

E van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B. Generations of ESTs from sprouting potato eyes

Unpublished (2000)

Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various Sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG598154 659 bp mRNA EST 12-APR-2001
EST496832 CSTS Solanum tuberosum CDNA clone CSTS20M23 5' sequence,
mRNA sequence.
                   GGTGACTCGGTTTCTTCACGATTATGGAGTCTGTCGGAGATCATCCGCATTCCGCTCAT 342
                                                                                                                                                              343 AAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCCGCCGATAGTC 402
                                                                                                                                                                                                       241 GACCATCCGCGTAAGGCTAAGGATTTTTATCACTTTGTTCCTAAGTTAGGGGAACCTAAG 300
                                                                                                       TCATGCAATCTAATCTACCCTCTATCGCCGGAGAAAATGCCGGAGTTCCGGTATCAGAAC
                                                                                                                                                                                                                                                  GAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACTCTGTTTCCCGGT
                                                                                                                                                                                                                                                                                         301 GATGCACCGGGGGTCCAACTAGCCCCGCTCTTAGCCCATTCAGGTGACACTTTTTCCGAAT
                                                                                                                                                                                                                                                                                                                                  CGCGGGGTGTGCATCGGAATAACGACGCACCACCGTTAGCGATGCTCCATCGTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                       523 GGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGATGAATTCTT 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host~"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .659
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cs7s20M23"
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Best Local Similarity
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BG598154
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KEYWORDS
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Alcalad, Vreballov, J., White, R., van der Hoeven, R.S., Holt, I.E.,
Liang, F., Hansen, T. S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales, Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                  EST405335 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG15H6, mRNA sequence.
BE434257
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                                                                                                                                                                                                                                                                                                            24-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation of ESTs from tomato fruit tissue, breaker stage Unpublished (2000)
Contact: David Frisch
Clemson University
Tol Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4356
Fax: 864 656 4359
Email: dfrischeCLEMSON.EDU
                                      377 TTGGCACAACCTAAGGATGCACCGGGGGTCAAACTAGTCCCGGTCTTAGCCATTCAAGTG
                                                                               ACTCTGTTTCCCGGTCGCGGGTGTGCATCGGAATAACGACGCACCACCGGTTAGCGAT
CTGCCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTG
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/clone="cLEG15H6"
/clone_lib="tomato breaker fruit, TIGR"
/tissuc_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"

    591
    /organism="Lycopersicon esculentum"
/cultivar="TA496"

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52.7%; Pred. No. 5.1e-14;
Live 0; Mismatches 225;
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Location/Qualifiers
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Matches 251; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanales; Solanaceae; Solanum;
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Jaclata, Vrebalov, J., White, R., van der Hoeven, R.S, Holt, I.E.,
Liang, F., Hansen, T. S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Glovannoni, J.J., Martin, G.B. and Tanksley
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                                                                         CTCGATTTCGTTCAAACCATTATTCCTACTCTTAAACATTCACTCTCCCTCACTCTCAAA
                                                                                                                                                                                                                                   TTCCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCAT
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                                                                                                                   CCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTCAAA
                                                                                                                                                                          CACTICITCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCGGAG
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                             GCGCCACCTCCCCACGCGCGCGCACAGAGCTAACGCTCCCTCTAACTTTTGATCT -
                                                                                                                                                                                                                                                                                                                                                       CTGCCGCCGATAGTCGAAGTTCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW650280 518 bp mRNA EST 04-APR-2
EST328734 tomato germinating seedlings, TAMU Lycopersicon
esculentum cDNA clone cLEI12F13 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:7411518
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Contact: David Frisch
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GATGAACAGTGCTT 659
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AW650280.1
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SOURCE
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/db_xref="taxon:4081"
/clone="role112F13"
/clone="to.E112F13"
/clone="to.E112F13"
/clone_lb="to.enato germinating seedlings, TAMU"
/tissue_type="whole seedlings"
/dev_stage="7 days post imbibition"
/note="vector: pBlueScript SK(*); Site_1: EcoR1; Site_2:
/note="vector: pBlueScript SK(*); Site_1: EcoR1; Site_2: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 487)
van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang
,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W.,
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST307245 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT1D15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 TGGCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAACCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 CATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 CTGTTTCCCGGTCGCGGGGTGTGCATCGGAATAACGACGCACCACCACCGTTAGCGATGCT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GATTTCCTTCAAAACATTATTCCTCTCTTAAAAATTCACTCTACCTCTCTCAAACAC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 GCTACTATAAACAGGGTCCATAAAGGCGTGGGCGTCTACTCCACAAATTCGGTGGACATGAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGGTTAGGGTTTCGCCGTATGAGGCGGATATTTTTACAAGCTCTCCATTATCAAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCTCAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 TICTICCCCCTTTCATGCAATCTACCCTCTATCGCCGGAGAAATGCCGGAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 CGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGATCATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 TATCTCATTGGTGACCATCCGCGTAAGGCTAAGGATTTTGATCACTTTGTTCCTAAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 CCGCCGATAGTCGAGGAATCTGATCGGAAATTGTTTCAAGTTTTAGCCGTGCAAGTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 CCATCGTTTGTAGGGTTTATGAAGAGTTGGGCTTCCATCACTAAATTCGGAGGAGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 112; DB 119;
51.8%; Pred. No. 3.4e-13;
tive 0; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW616206.1 GI:7322240
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Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon.
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Liang, F.,

Tracheophyta;

JOURNAL

COMMENT

TITLE

FEATURES

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/note="Vector: pBluescriptSkmcUadapt; Site_1: 5' EcoRI; Site_2: % XhoI; Roots were harvested from plants grown under the following deficiencies/stresses: 10 mM Al, Zn, P, K, Fe,N. mRNA was isolated from indivdual treatments. Proportional aliquots of mRNA of each treatment were mixed and used for library construction."
                                                                                                                                                                                           1 (bases 1 to 482)
van der Hoeven, R.S., Garvin, D.F., Matern, A.L., Holt, I.E., Liang, F., van der Hoeven, R.S., Rarvin, D.F., Matern, M.B., Bowman, C.L., Upton, J., Hansen, T.S., Ronning, C.M., Craven, M.B., Bowman, C.L., and Tanksley, S.D. and Tanksley, S.D. Giovannoni, J.J. Generation of ESTs from tomato nutrient-deficient roots Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 AAACCCGATTTCGTTCAAAA:ATTATTCCTCTCTTAAAAATTCACTCTCCCTCACTCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACACTTCTTCCCCCTTTCATGCAATCTAATCTACCCTCTATCGCCGGAGAAATGCCG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 CATCCGCATTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 CAAGTIGGGCCACCICCGGGGGGGCAACGGAGGTGAIACICCCTCITACITAITITGAC 66
                                                                                                                        core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 CGAGTGGCGCCCTCCAGGCACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AAACCCGCCTTCCTCGAAACCGTCGTTCCGAAACTCAAACAATCCTTATCTCTAACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTICCGGTATCAGAACGGTGACTCGGTTTCTTTCACGATTATGGAGTCTGTCGGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GAGTTACGTTATGTGACAGGNGATTCTGTGTCTGTTACTTTTTCGAGACTGATATGAAT
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                                                                                              Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 144; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deficient roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106.8; DB 144; Lengt
Pred. No. 4e-12;
0; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organish="Lycopersicon esculentum"
/cultivar="TA492"
/db_xref-"taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_11.b="tomato nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots"
/dev_stage="5-6 weeks old"
/lab_host="Soln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: dfrisch@CLEMSON.EDU.
Location,/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cLEW18020"
                                                                          Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.0%;
Best Local Similarity 51.7%;
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Öl
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                              ycopersicon.
                                                tomato
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                                                SOURCE
                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                       AUTHORS
                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                        /organism="Lycopersicon hirsutum"
/db_xref="taxon:62890"
/db_xref="taxon:62890"
/clone="cLHTD15"
/clone=lib="L. hirsutum trichome, Cornell University"
/tissue_type="mixed stages"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
nitrogen, shearing off trichomes. This procedure yielded a
mixture of cells which is highly enriched for trichome
likely with minor contaminations of other types of leaf
cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TTTGTTCAAAAACATTATTCCTCCTCTTAAAAATTCACTTTCCCTCACTCTCAAACACTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 GCTGCATTTCCACCCCATGCTTCAGCTTCTTCTACGAACTCCCCTGTTCCAAACCGC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         333 TTCCGCTCATAAATACTACTGCTTTGCCCCTAGCGACGATTATGAAGATCTCCAGCTGCC 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 TCTCATTGGCGACCATCCGCGTAATGCTAAGGATTTTTATCACTTTGTTCCTAAGTTAGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from wild tomato (Lycopersicon hirsutum) trichomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 GCCGCCTCCAGGCACGGTGGCTGAGCAGTCACTCCCGCTCACCTTCTTCGACATGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TATGCCCTTAGCCGGAACGTTGCTTGTCCACTAGATACAAACGGATATCCTGAGTTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 118;
                                                                                    Unpublished (2000)
Contact: David Frisch
Contact: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 7.1%; Score 10%; DB 116 al Similarity 51.7%; Pred. No. 2.3e-12. 246; Conservative 0; Mismatches 230
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Query Match

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                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

( thases 1 to 456)

van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougti, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B.

Generation of ESTs from potato leaves and petioles
                                                                                                            BEST1273 456 bp mRNA EST 02-OCT-2000 CST027341 potato leaves and petioles Solanum tuberosum.cDNA clone EST282609 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             For clone request: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com. Location/Qualifiers
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/tisue_type="leaflets and petioles"
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Contact: Cathy Ronning
The Institute for Genomic Research
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AL418128 T3 end of
A16155 PTOM36. 10/
A20628 PTOM36 frag
AR003699 Sequence
IZB271 Sequence
AR110778 Sequence
AR110778 Sequence
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53 CNS06W8Q
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces narxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See the other extremity of this insert.
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KPTWLSIVSTNIRNVCILLDOTKDGEGFEAMITLSEEDMSWFESDERVLEFAQVNPGVT
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Souciet,J.L., Aigle,M., Artiguenave,F., Casaregola,S.,
Belotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
Benontigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozler-Kalogeropoulos,O., Potler,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
yeast species for molecular evolution studies(1)
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; Pichia.

1 (bases 1 to 915)
de Montigny, J., Spehner, C., Souciet, J., Tekaia, F., Dujon, B., Wincker, P., Artiquenave, F. and Potier, S.
Genomic Exploration of the Hemiascomycetous Yeasts: 15. Pichia
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Location/Qualifiers
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Euphorbia esula F21J9.20-like protein mRNA, partial cds.
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/dev_stage="3-day induced (defoliated)"
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/clone="12a"
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Unknown.
Unclassified.
1 (bases 1 to 1080)
Bird,C.R., Boniwell,J.M., Grierson,D., Ray,J.A. and Schuch,W.W.
Transformed tomato plants
Patent: US 5569829•A 1 29-OCT-1996;
                                                                                                                                                                                                                         Unknown..
Unclassified.
Unclassified.
1 (bases 1 to 1080)
Bird,C.Roger, Grierson,D., Ray,J.Anthony and Schuch,W.Walter.
PTOM36 constructs and tomato cells transformed therewith
Patent: US 5744364-A 1 28-APR-1998;
Location/Qualifiers
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Pred. No. 9e+02;
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                                                                                              2 others
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Pred. No. 9.1e+02;
2; Mismatches 2;
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/db_xref="taxon:32630"
141 c 208 g 375 t
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/db_xref="taxon:32630"
141 c 208 g 375 t
        /organism="Pichia farinosa"
/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AxXOAA029C10"
/clone_lib="AXXOAA"
/note="end : T3"
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KEYWORDS
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1 (bases 1 to 1320)

St-Pierre, B., Laflamme, P., Alarco, A.M. and De Luca, V.

The terminal O-acetyltransferase involved in vindoline biosynthesis defines a new class of proteins responsible for coenzyme A-dependent acyl transfer plant J. 14 (6), 703-713 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-MAR-1998) Institut de Recherche en Biologie Vegetale, 4101 Sherbrooke East, Montreal, QC H1X 2B2, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          AFU53307 1320 bp DNA PLN 01-JAN-1999
Catharanthus roseus deacetylvindoline 4-0-acetyltransferase (DAT)
gene, complete cds.
                                                                                                                                                                                                                                                                                                                              Gaps
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/product="deacetylvindoline 4-0-acetyltransferase"
/protein_id="AAC99311.1"
/db_ref="GI:4091808"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="deacetylvindoline 4-0-acetyltransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="involved in the last step in vindoline biosynthesis"
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17-0-acetyltransferase"
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Pred. No. 9e+02;
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/cultivar="Little Delicata"
/db_xref="taxon:4058"
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St-Pierre, B., Laflamme, P. and De Luca, V.
Direct Submission
                                                                                                                1 (bases 1 to 1096)
Atkinson,R.L. and Dhurandhar,N.V.
Viral obesity methods and compositions
Patent: US 6127113-A 1 03-0CT-2000;
                                                                                                                                                                                                                                                                                                               9e+02;
                                                                                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                              2; Mismatches
Sequence 1 from patent US 6127113.
ARI10778
                                                                                                                                                                                                               /organism="unknown"
215 c 227 g
                                                                                                                                                                                  Location/Qualifiers
                                    GI:12827626
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76.5%;
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                                                                                                 Unclassified
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Best Local Similarity
                                     AR110778.1
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Unknown.
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/translation="MESCKISVETETLSKTLIKPSSPTPQSLSRYNLSYNDQNIYQTC
VSVGFFYENPOGIELSTIREQLQNSLSKTLVSYYPRGKVVKNDZIHCNDDGIEFVEV
RTCRMNDILKYELRSYRADLVLDKRYVGSEDFTAIVQLSHFDGGGLAVARGISHKV
ADGGTTASFMKDWA-SAGNYLSSSHHVPTPLLVSDSIFPRODNIICEOFPTSKNOVEKT
FIFPPEAIEKIKSKAVEFGIEKPTRVEVLTAFLSRCATVAGKSAAKNNNCGQSLPFPV
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SREKLTYVAQMEEFVBSTIKENDYLNSTSSWCRFPFYDVDFGWGKPIWVCLF
OPYIKNOVVMMDYFFGDDYGIENFLDIDAYLSDSWCRFPFYDVDFGWGKPIWVCLF
OPYIKNOVVMMOYPFGDDYGIENTSEDENSAFEKNEQLLGFVSN"

244 C 252 g 415 t
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ARSORVSVSADPAKTIREALSKVLVYYPPFAGRIRWTENGDLEVECTGEGAVFVEAMA
DNDLSVLQDFNEYDSPFQOLVFNLREDVNIEDLHLITVQVYRFTGGGFVVGTRFHFSV
SDGKGTGOLLKGWGBRARGERKPSLEPIWNREMVKPEDIMYLQFDHFDFIHPPLNLGR
SIQASWYISFERINYTKRCMMEECKEFSAFEVVVALIWLARTKSFRIPPNBYVKIIF
FIDMRNSFSDSPLBKGTYGANIGNACAMDNYRDLLNGSLLYALMLIKKSKFALNENFKS
RILTRFSTLDANMKHENVVGGGDWRNIGFYEDDFGGRONAVNYSPMQOOREHELAMQNY
FLFLRSAKNMIDGIKILMFMPASMYKPFKIEMEVTINKYVAKICNSKL
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Direct Submission
Submitted (20-AUG-2000) Institute of Biological Chemistry,
Washington State University, PO Box 646340, Pullman, WA 99164-6340,
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1 (bases 1 to 1388)
Walker,K. and Croteau,R.
Taxol biosynthesis: Molecular cloning of a benzoyl- CoA:taxane 2alpha -0-benzoyltransferase CDNA from Taxus and functional
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Proc. Natl. Acad. Sci. U.S.A. 97 (25), 13591-13596 (2000)
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/product="2-debenzoyl-7,13-diacetylbaccatin
III-2-0-benzoyl transferase"
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Pred. No. 8.8e+02;
2; Mismatches 2;
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Pred. No. 8.8e+02;
2; Mismatches 2;
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/db_xref="taxon:99806"
22. .1344
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76.5%;
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| 1138 GATTTTGGATGGGGAAA 1154
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Best Local Similarity 76.5
Matches 13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
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DEFINITION

RESULT 1 AF190130

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

TITLE

FEATURES

gene

MEDLINE PUBMED

REFERENCE AUTHORS

JOURNAL

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/translation="modotaceritikpsspapohostyklsiiddltyvesiilly
skagestaktsohilkeslsnylthyyplagokyydolivdgoppieahyyddag
ollininiuuubedllepshefebbsnylthyyprecegamiglepshylddag
affikinduubedlepshefebbsnylthyydynyrecegamiglepshyldhya
affikindylargagerkuyiidhaslepardlsclyrsydeefelkeseftreyebb
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rmnpppfehgmiisgglyymplekkuygclareihesikkydgofarfygdebe
egverawglepredenyskrefewytswcktplyfadegenymplekebbssde
egverawgleprromarfeknosgilaytsphpsif"

280 c 320 g 426 t
                                                                                                         Tunen, A.J.
Fruit flavour related genes and use thereof
Patent: WO 0032789-A 38 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tunen, A.J.
Fruit flavour related genes and use thereof
Fruit flavour related genes and use thereof
Patent: WO 0032789-A 44 08-JUN-2000;
AHARONI ASAPH (IL); VERHOEVEN HARRIE ADRIANUS (NL); LUECKER JOOST
(NL); CPRO DLO (NL); CONNELL ANN PATRICIA O (NL); TUNEN ARJEN
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 1436)
Aharoni,A., Verkoeven,H.A., Luecker,J., O'Connell,A.P. and Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1471)
Aharoni,A., Verhoeven,H.A., Luecker,J., O'Connell,A.P. and Van
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Pred. No. 8.8e+02;
2; Mismatches 2;
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Sequence 44 from Fatent WO0032789.
AX025518
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/codon_start=1
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/db_xref="GI:10187183"
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                                                                                                                                                                                                                                                           1. .1436
/organism="Citrus limon"
/db_xref="taxon:2708"
34. .1314
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/db_xref="taxon:3656"
                                                                                                                                                                                                                 JOHANNES VAN (NL)
Location/Qualifiers
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                   /note="cDNA
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Best Local Similarity 76.5
Matches 13; Conservative
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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                                                                                                                                                                       Taxus cuspidata taxadienol acetyl transferase (TAT) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1419)
Walker,K., Schoendorf,A. and Croteau,R.
Walker,K., Schoendorf,A. and Croteau,R.
Submission (24-SEP-1999) Institute of Biological Chemistry, PO Box 646340, Pullman, WA 99164-6340, USA
                                                                                                                                                                                                                                                                                                                                        Conferopsida; Conferales; Taxaceae; Taxus.

( bases 1 to 1419)

Walker,K., Schoendorf,A. and Croteau,R.

Walcelar cloning of a taxa-4(20),11(12)-dien-5alpha-ol-0-acetyl
transferase cDNA from Taxus and functional expression in
Escherichia coli
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/protein_ld="AAF34254.1"
/db_xref="G1:6978038"
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20132877
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Pred. No. 8.8e+02;
2; Mismatches 2;
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/organism="Taxus cuspidata"
/db_xref="taxon:99806"
1. .1419
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Sequence 38 from Patent WO0032789.
AX025512. GI:10187182
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76.5%;
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11. .1330
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1120 GATTTGGATGGGGAAA 1136
                                                                                                                                                   1419 bp
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    1 GAYTTYGGNTGGGGNAA 17
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Best Local Similarity 76.5
Matches 13; Conservative
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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1 GAYTTYGGNTGGGGNAA 17
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               DADVSLEEFWDTLPYSLSSMONNITHNALNSDEVLNSPLLLIQVTRLKCGGFIFGLCF
NHTMADGFGTVQFWRATAEIARGAFAPSILVWQRALLTARDPPRITFRHYEYDQVVD
MKSGLIPVNSKIDQLFFFSQLQISTLRQTLPAHLHOCOFFEVLTAYVWRLRTTALQFK
PEEBYRFLCWWNLRSKIDIPLGYPVOYDVITTARAKA
ATMEYIKSTVDLMVIKCRPYFFVVGSPMASDLTRIGYENVDFGWGRALFGGPFTTGAR
ITRGLVSFCVVFMNRNGEKGTALSLCLPPPAMERFRANVHASLQVKQVVDAVDSHMQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-JUN-1999) to the DDBJ/EMBL/GenBank databases. Keiko Y Sakakibara, Suntory Research Center, Fundamental Research, Plant Biotech; Shimmamoto-cho, Wakayamadai, 1-1-1, Mishima-gun, Osaka 618-8533, Japan (E-mail:Keiko_Sakakibara@suntory.co.jp, Tel:+81-75-962-8807, Fax:+81-75-962-8262)
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HHTVSDAPSFLAFITAWSSMSKHIENEDEDEEFKSLPVFDRSVIKYPTKFDSIYWRNA
LKFPLQSRHPSLPTDR.RTTFVFTQSKTKKLKGWIQSRVPDRSVHLSSFVALAAXWWAG
LKFPLQSRPSLPDR.RTTFVFTQSKTKKLKGWIQSRVPSLVHLSSFVALAAXWWAG
LTKSFTADEDQDNEDAFFLIPVDLRPRLDPPVPENYFGGNCLSYALPRWRRELVGEKG
VFLAARIYRABIKRIDFTURWSPBIRKALOKSYFSVAGSSKLDLVGADFGW
GKARKQEILSIDGEKYAMTLCKARDFEGGLEVCLSLPKDKMDAFAAYFSLGING"
315 c 331 g 411 t
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/protein_id="BAA93475.1"
/db_xref="di:7415646"
/db_xref="di:7415646"
/translation="VETCRVGPPDDSVAEQSVPLTFFDMTWLHFHPMLQLLFYEFPC
SKQHFSESIVPKLKQSLSKTLIHFFPLSCNLIYPSSPEKMPEFRYLSGDSVSFTIAES
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NIYPHNPSLEGRDPVKVIKEAIGKALVFYYPLAGRLREGPGRKLFVECTGEGILFIEA
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1 (sites)
Sakakibara, K.Y., Tanaka, Y., Mizutani, M.F., Fujiwara, H., Fukul, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB029340 1476 bp mRNA PLN 04-APR-2000 Perilla frutescens mRNA for anthocyanin acyltransferase, partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashikari,T., Yamaguchi,M. and Kusumi,T.
Molecular and biochemical characterization of a novel
hydroxycinnamoyl-CoA: anthocyanin 3-0-glucoside-6
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76.5%; Pred. No. 8.7e+02;
11ve 2; Mismatches 2;
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/db_xref="taxon:48386"
/tissue_type="leaf"
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2 (bases 1 to 1476)
Sakakibara,K.Y. and Tanaka,Y.
Direct Submission
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F1 FUNUL YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
C12R1:865),
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Senecio cruentus mRNA for acyltransferase, partial cds.
E12757 E12757
JP 1997070290-A/5.
                                                                                                                     24 - JUN - 1998
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PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 19691
ASHIKARI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI
MASAHIRO,
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unidentlied
unclassified.
1 (bases 1 to 1508)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
                                                                                                                                                                                                                                                                              1 (bases 1 to 1479)
Ashikari,T., Tanaka,Y., Fujiwara,H., Nakao,M., Fukui,Y.,
Yonekura,K., Mizutani,M. and Kusumi,T.
GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
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Perilla ocimoides mRNA for acyltransferase,partial cds.
E12756
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Location/Qualifiers
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76.5%; Pred. No. 8.7e+02;
iive 2; Mismatches 2;
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SUNTORY LTD
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/organism="unidentified"
/db_xref="taxon:32644"
a 316 c 331 g 41:
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JP 1997070290-A/4
18-MAR-1997
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1167 GATTTTGGATGGGGGAA 1183
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GENE CODING PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY
PALENT: JP 1997070290-A 5 18-MAR-1997;
SUNTONY LID
SUNTON DE 1997070290-A/5
PD 18-MAR-1997
PF 30-JAN-1996 JP 1996046534
PF 30-JAN-1996 JP 1996046534
PR 17-FEB-1995 JP 95P 67159, 29-JUN-1995 JP 95P 196915 PI
ASHIRANI TOSHIHIKO, TANAKA YOSHIKAZU, FUJIWARA HIROYUKI, PI NAKAO
PI PUKUI, YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI JAKAAKI PC
                                                                                                                                                                                                             I FUKUI YUKO, YONEKURA KEIKO, MIZUTANI MASAKO, KUSUMI TAKAAKI PC
C12N15/09,A01H1/00,C07H21/04,C07K14/42,C12N9/10,(C12N9/10, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.5%; Pred. No. 8.7e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                              1. .1508
/organism='Senecto cruentus'
/tissue_type='petal'
/clone='pcAT48'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-'acyltransferase'.
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 1508
/organism="unidentified"
/db_xref="taxon:32644"
a 293 c 296 g 477
                                                                                                                                                                                                                                      C12N15/09, A01H1/00, C07H21/C
C12R1:865), PC (C12N9/10, C12R1:19); CC strandedness: Double; CC topology: Linear; FH Key Location FT source 1. .150E FT CDS (C15Sue_FT CDS T) (P1367 FT CDS T) (Product FT CDS T) (Product FT CDS T) (Product FT CDS T)
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ORIGIN
      TITLE
JOURNAL
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                                                                  COMMENT
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Search completed: November 5, 2001, 16:58:20 Job time: 11270 sec

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Geranylgeranyl dip
Clone pTOM36. Lyc
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Arabidopsis thalia
Lemon alcohol acyl
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Arabidopsis thalia
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                                                                                               ; Search time 445.49 Seconds (without alignments) 23.961 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / SIDSI/gcgdata/geneseq/geneseqn/Na1980.DAT:*
/ SIDSI/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      730101 seqs, 313950809 residues
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AAQ11802
AAQ46682
AAV07891
AAC49764
AAC339128
AAC33113
                                                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                                      Scoring table:
                                                                 OM nucleic
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Aromatic acyl tran Malon ripening-rel Anther specific CD Aromatic acyl tran Aromatic acyl tran Aromatic acyl tran Arabidopsis thalia Arabidopsis thalia Anther specific ge Tobacco Ant32 geno Human gene express Human gene express Human gene express Human serceted pro Human serceted pro Human colon cancer Streptococcus pneu Human colon cancer Streptococcus pneu Human colon cancer Neisseria meningit Arabidopsis thalia Arabidopsis concinna b Clarkia concinna b	concinna occus pne gitidis p
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1508 1518 1526 1526 1605 17622 17622 17622 17622 17622 17622 17622 17622 17622 17622 17622 17622 17632 1764 1764 1764 1764 1764 1764 1764 1764	473 934
77777777777777777777777777777777777777	
C C C C C C C C C C C C C C C C C C C	4 4 4 5 4 5

ALIGNMENTS

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Degenerate primer for identifying aromatic acyl transferase sequence.
                                                                                            Aromatic acyl transferase: transformation; anthocyanin pigment; plants; acylation; colour: tone; colouration; colour change; gentiana triflora; Petunia hybrida; Perilla ocimoides; scenecio cruentus; Lavandula angustifolia; ss.
                                                                                                                                                                 Location/Qualifiers
                  AAT37314 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                      95JP-0046534.
95JP-0067159.
95JP-0196915.
                                                                                                                                                                                             /mod_base= I
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/mod_base= I
                                                                                                                                                                                                                                                                                   96WO-JP00348.
                                                        (first entry)
                                                                                                                                                                                     Ø
                                                                                                                                                                                     /*tage
                                                                                                                                                                                                                                                                                                     30-JAN-1996;
17-FEB-1995;
29-JUN-1995;
                                                                                                                                                                        misc_feature
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                    16-FEB-1996;
                                                        06-FEB-1997
                                                                                                                                                                                                                                              WO9625500-A1
                                                                                                                                                                                                                                                                 22-AUG-1996
                                                                                                                                              Synthetic.
                                    AAT37314;
        AAT37314
RESULT
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a

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Gaps

; 0

Length 23; Indels

DNA

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The present sequence represents a PCR primer for a geranylgeranyl achieves by synthase has cytostatic activity. A vector encoding GGPP synthase is useful in increasing GGPP synthase levels in a host cell preferably Taxus (Yew) cell and thereby facilitates production, isolation and purification of larger amounts of GGPP synthase is useful in obtaining expression or enhanced expression of GGPP and other diterpenes, such as pacilizat, useful as anticancer drugs. Isolated nucleic acids encoding GGPP synthase or hybridising with GGPP synthase encoding nucleic acids are used for identifying genes encoding GGPP synthase from microorganisms such as Taxomyces andreane and Penicillium raistrickii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is contained in a DNA construct used to transform host plant cells for regulating the prodn. of the enzyme encoded by pTOM36. Plants such as apple, tomato and mango may be modified to produce e.g. sweeter fruit, novel flavour, modified colour or to have improved processing characteristics. The DNA construct pref. also comprises a constitutive or regulatory promoter, e.g. the CaMV 35S or poly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA constructs contg. DNA from proM36 clone - used to transform plants to regulate prodn. of the fruit-ripening proM36 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1080 BP; 357 A; 141 C; 207 G; 375 T; 0 other;
                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 12;
Pred. No. 74;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                          Sequence 23 BP; 6 A; 9 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                              Score 14.2; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ray JA, Schuch WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ11802 standard; DNA; 1080 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ICIL ) IMPERIAL CHEM INDS PLC
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                                                                                                                                                                                                                                                                              83.5%;
76.5%;
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Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fruit ripening; pTOM36; ss
                                                                                                                                                                                                                                                                                                                                                   GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                            Local Similarity 76.5
les 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  20 GATTTCGGCTGGGGTAA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone pTOM36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9105865-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA011802;
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Best Local S
                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Geranylgeranyl diphosphate synthase; GGPP synthase; yew; cytostatic; anticancer; Taxus; diterpene; paclitaxel; identification; plant; Taxomyces andreanae; Penicillium raistrickii; microorganism;
                                                                                                                                                                                                                                                      with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-173131. This degenerate primer was synthesised base on a peptide fragment (AAW04728) isolated from three of the six clones. It was used to identify
                                                                                                                                       plants
tone,
                                                                                                                                                                                                                                         Vectors containing DNA fragments encoding proteins of plant origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                   coding for aromatic acyl transferase - for transforming the produce anthocyanin pigments and thus altering colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.5%; Score 14.2; DB 17; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geranylgeranyl diphosphate synthase PCR primer SEQ ID NO:6.
                                                 Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                      other aromatic acyl transferase encoding clones
                                           I, Fujiwara H, Fukui Y, Kusumi T,
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 BP; 3 A; 0 C; 7 G; 3 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Column 39; 57pp; English.
                                                                                                                                                                                                      Claim 3; Page 82; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.00,
100.08; FAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                             Ashikari T, Fujiwara H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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            (SUNR ) SUNTORY LTD.
                                                                                                WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taxus canadensis.
                                                                                                                                                                    e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6043072-A
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                                                               Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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Gaps

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Length 1080;

AAQ46682;

AAQ46682

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Nucleotide sequence of the fiber protein encoded by adenovirus Ad-36p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence encoding the adenovirus Ad-36p fiber protein used in the method of the invention to determine if a person is suffering viral obesity. The method is used to determine whether obesity in a person has a viral basis. Ad-36p can be used as a basis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining if obesity in a person is caused by Ad-36 virus - and providing the basis for treatment or prevention of obesity-causing, cholesterol reducing adenovirus, using the purified variant, Ad-36p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1096;
                                   Adenovirus; Ad-36p fiber protein; viral obesity; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1096 BP; 353 A; 215 C; 227 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 62347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                           /*tag= a
/product= "Ad-36p fiber protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DE
Pred. No. 74;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obesity in a person has a viral basis. Ad-3 of a vaccine to prevent viral-based obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Pages 18-19; 24pp; English.
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.5%;
76.5%;
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99US-01231E0.
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| 1013 gattttggatggggtaa 1029
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Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                        1..1096
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                                                                       Mastadenovirus
                                                                                                                                                                                                                                                                                                                                                                                Atkinson RL,
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05-MAR-1999;
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                                                                                                           Key
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                                                                                                                                                                                                                                                                     Transgenic fruit production; prodn.; increased solids content; higher reducing sugar content; tomato; tomatoes; plant cultivation; improved; paste; soup; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic fruit with increased solids content - is obtd. by cultivating plants, esp. tomatoes, in which expression of genes homologous to prOM36 is inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.5%; Score 14.2; DB 14; 76.5%; Pred. No. 74;
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                                                                                                                        AAQ46682 standard; cDNA; 1080 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   improved tomato paste and soup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV07891 standard; cDNA; 1096
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|866 gattttggatggggaaa 882
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866 gattttggatggggaaa 882
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1 GAYTTYGGNTGGGGNAA 17
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Matches 13; Conservative
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                                                                                                                                                                                                                                   pTOM36 cDNA clone
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Bird CR,

AAV07891;

RESULT
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Query Match

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	900S-012 900S-012 900S-012 900S-012 900S-012 900S-013 900S-013	10 - SAN	908 - 013 - 014 -
990x - 0123548 990x - 0125624 990x - 0126264 990x - 0126264 990x - 01276785 990x - 0128714 990x - 0128714 990x - 0130047 990x - 0130047 990x - 0131449 990x - 0131449 990x - 0131486 990x - 0131486 990x - 0131486 990x - 0131486 990x - 0131486 990x - 0131487 990x - 0131486 990x - 013186 990x - 014089 990x - 014089 990x - 014089 990x - 014089 990x - 014089 990x - 014089 990x - 014089	09-MAR-1999 23-MAR-1999 25-MAR-1999 01-APR-1999 06-APR-1999 06-APR-1999 16-APR-1999 11-APR-1999 21-APR-1999	23-APR 1999 23-APR 1999 30-APR 1999 30-APR 1999 05-MAY 1999 06-MAY 1999 06-MAY 1999 11-MAY 1999 11-MAY 1999 11-MAY 1999 11-MAY 1999 12-MAY 1999 22-MAY 1999 22-MAY 1999 03-JUN 1999 03-JUN 1999 04-JUN 1999	PR 10-70N-1999; PR 110-70N-1999; PR 14-70N-1999; PR 16-70N-1999; PR 16-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 18-70N-1999; PR 23-70N-1999; PR 23-70N-1999;

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990'S - 0130'84'9,
990'S - 0130'89'10'
990'S - 0131'84'9,
990'S - 0132'40'7,
990'S - 0132'48'7,
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990'S - 0132'88'7,
990'S - 0134'21'8,
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990S-0135523.
990S-0135629.
990S-0136021.
990S-0136392.
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990S-0140991.
990S-0141287.
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990S-0142154.
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99US-0144005.
99US-0144085.
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99US-0144331.
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990S-0139817
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99US-0140353
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61 - JUN - 1999
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21 - 70N - 1999;
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24-JUN-1999;
28-JUN-1999;
29-JUN-1999;
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01-JUL-1999;
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15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                        Length 1427;
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                                                                                                                                                                                                                                                                                                                                         DB 21;
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Pred. No. 76;
2; Mismatches
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990S-0157865.
990S-015812029.
990S-015813123.
990S-015813123.
990S-0159293.
990S-0159293.
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990S-0159331.
990S-0159331.
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990S-01611360.
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990S-012548.
990S-0126264.
990S-0126785.
990S-012762.
990S-012834.
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76.5%;
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1161 gatttcggttggggtaa 1177
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nes 13; Conservative
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05-MAR-1999;
09-MAR-1999;
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Best Local S1
Matches 13;
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990S-0144632.
990S-0144884.
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990S-0145086.
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990S-0147303.
990S-0147416.
990S-0147493.
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99US-0154779
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02 AUG 1999
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15-SEP-1999;
16-SEP-1999;
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24-SEP-1999;
28-SEP-1999;
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20-AUG-1999;
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25-AUG-1999;
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06-0CT-1999;
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08-0CT-1999;
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01-SEP-1999,
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10-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strawberry; fruit flavour; biosynthetic pathway; aliphatic; thiolase; aromatic ester; alcohol acyl transferase; alcohol dehydrogenase; pyruvate decarboxylase; aminotransferase; esterase; alcohol; aldehyde; alpha-keto acid; amino acid; fatty acid; acyl-Coh; processed food; food additive; flavour; syrup; ice-cream; frozen dessert; yoghurt; confectionery; flavouring; oral medication; vitamin; aroma; beverage; alcohol; scent; fragrance; perfume; cosmetic; suspension aid; aluminium salt; anti-perspirant; pharmaceutical; cleaning product; insect pheromone; day carrier; solvent; insect repellent; miticide; scablcide; plasticiser; deodorant; ss.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Connell AP;
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                     Length 1429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lemon alcohol acyl transferase encoding cDNA SEQ ID NO:20A.
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Tunen AJ,
                                                                                                                                                                                                                                                                                     Score 14.2; DB 21;
Pred. No. 76;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aharoni A, Luecker J, Verhoeven HA,
                                                                                                                                                                                                                                                                                                                                                                                                           AAC64784 standard; cDNA; 1436 BP.
                                       9905-015958
9905-0159584
9905-0160767
9905-0160767
9905-0160768
9905-0160814
9905-0160815
9905-0160981
9905-0160981
9905-0160981
9905-0161406
9905-0161406
                                                                                                                                                                                                                                                                                     83.5%;
76.5%;
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99EP-0200739.
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99US-0161920
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1163 gatttcggttggggtaa 1179
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                                                                                                                                                                                                                                          99US-0161992
99US-0161993
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                 1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                Local Similarity 76.5
les 13; Conservative
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P-PSDB; AAB36458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Citrus limon.
                 14-007-1999
14-007-1999
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21-007-1999
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Matches
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alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, aminotransferase and esterase activities, which are involved in the bisynthetic pathway for allohal dehydrogenase, pyruvate decarboxylase, aminotransferase and esterase activities, which are involved in the bisynthetic pathway for allohalic and/or aromatic ester production in fruit. The nuclectide sequences can be inserted into the genome of a fruit-producing plant to regulate allohatic end/or aromatic ester formation. Aromatic and/or allohatic esters in microorganisms, plant cansferase are produced by inserting thiolase, alcohol acyl ransferase and esterase nuclectide sequences into the genome and feeding the microorganism or plant with alcohol, aldehydes, alpha-keto acids, or amino acids and fatty acids, and acyl-CoA. The nuclectides and their proteins can be used in the processed food industry as food additives to enhance the flavour of syrups, ice-creams, frozan desserts, yoghurts and confectionery. They are used: as flavouring agents for oral medications and vitamins; provide flavour and aroma in beverages, including alcohol; enhance or reduce fruit flavour, aroma, fragrance or scent; enhance the flavour or aroma of natural, synthetic or artificial products; for the production of novel combinations of artificial flavour, profunce or partings and agents; as fragrance or partings of antificial flavour, and apprent or aroma of activity continues or partings of antificial flavour, and agents; as fragrance or partings of antificial flavour, and apprent or aroma or artificial flavour, and aroma or artificial flavour, and aroma or artificial flavour, and aroma or artificial flavour profunces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perfumes in cosmetics, creams, sun-protectant products, hair conditioners, lengthening agents and fixatives in perfumes, suspension adds for aluminium salts in anti-perspirant pharmaceuticals, cleaning products, personal care products and animal care products; as disinfectant additives; as degreasing solvents for electronics; as miticides, scabicides, plasticisers and decodorants. Insect repellents, maticides, scabicides, plasticisers and decodorants. The present sequence encodes lemon alcohol acyl transferase, from the present invention.
                              A new DNA sequence encoding a polypeptide with alcohol acyl transferase activity for producing and regulating aromatic and/or aliphatic ester formation in microorganisms, plant cells or plants
                                                                                                                                                                                                                                                       present invention describes nucleotide sequences with thiolase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1436 BP; 410 A; 280 C; 320 G; 426 T; 0 other;
                                                                                                                                                                           Example 5; Page 114-115; 163pp; English.
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A new DNA sequence encoding a polypeptide with alcohol acyl transferase activity for producing and regulating aromatic and/or aliphatic ester formation in microorganisms, plant cells or plants

O'Connell AP;

Verhoeven HA, Van Tunen AJ,

Aharoni A, Luecker J, WPI; 2000-412335/35

P-PSDB; AAB36461

activity

(CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD

99WO-NL00737. 98EP-0204018

02-DEC-1999; 02-DEC-1998; 12-MAR-1999;

08-JUN-2000

Gaps ö 83.5%; Score 14.2; DB 21; Length 1436; Indels 5, 2; Mismatches Pred. No. 76; 76.5%; 1 GAYTTYGGNTGGGGNAA 17 13; Conservative Query Match Best Local Similarity Matches Q ô

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Honey dew melon alcohol acyl transferase encoding cDNA SEQ ID NO:23A. AAC64787 standard; cDNA; 1470 BP 28-FEB-2001 (first entry) AAC64787; 6 AAC64787

Strawberry; fruit flavour; biosynthetic pathway; aliphatic; thiolase; aromatic ester; alcohol acyl transferase; alcohol dehydrogenase; pyruvate decarboxylase; aminotransferase; esterase; alcohol; aldehyde; alpha keto acid; amino acid; fatty acid; acyl-CoA; processed food; food additive; flavour; syrup; ice-cream; frozen dessert; yoghurt; confectionery; flavouring; oral medication; vitamin; aroma; beverage; aluminium salt; anti-perspirant; pharmaceutica; suspension aid; aluminium salt; anti-perspirant; pharmaceutical; cleaning product; insect pheromone; dye cariler; solvent; insect repellent; mittcide; scabicide; plasticiser; deodorant; ss.

Cucumis sp.

WO200032789-A1

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The present invention describes nucleotide sequences with thiolase, alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, alcohol acyl transferase, alcohol dehydrogenase, pyruvate decarboxylase, anicohol acyl transferase and esterase activities, which are involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit. The nucleotide sequences can be inserted into the genome of a fruit. The nucleotide sequences can be inserted into the genome of a formation. Aromatic and/or aliphatic esters in microorganism, plant cells or plants are produced by inserting thiolase, alcohol acyl minotransferase, alcohol dehydrogenase, pyruvate decarboxylase, aninotransferase and esterase nucleotide sequences into the genome and feeding the microorganism or plant with alcohol, aldehydes, alpha-keto additives to enhance the flavour of syrups, ice-creams, frozen desserts, caditives to enhance the flavour of syrups, ice-creams, frozen desserts, additives to enhance the flavour of syrups, ice-creams, frozen desserts, including alcohol; enhance or reduce fruit flavour, aroma, fragrance or scent; enhance the flavour or aroma of natural, synthetic or artificial products; for the production of novel combinations of artificial genes; as antibacterial or anti-fungal agents; as fragrance or perfumes in cosmetics, creams, sun-protectant products, as as suspension and along alcohol; enhance and dixatives in perfumes, suspension and softers, creams, sun-protectant products, as a series of a products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insect pheromones; and as dye carriers, solvents, insect repellents, mitlicides, scabicides, plasticisers and deodorants. The present sequence encodes honey dew melon alcohol acyl transferase, from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 23476.
                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 121-122; 163pp; English.
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99US-0140695

24 - JUN - 1999; 28 - JUN - 1999; 30 - JUN - 1999; 30 - JUN - 1999; 01 - JUL - 1999; 06 - JUL - 1999; 06 - JUL - 1999; 07 - JUL - 1999; 12 - JUL - 1999; 13 - JUL - 1999;

08-70L-1999; 09-70L-1999; 12-70L-1999; 13-70L-1999; 14-70L-1999; 15-70L-1999; 16-70L-1999; 16-70L-1999; 19-70L-1999; 19-70L-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999;

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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss
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990S-0139461
990S-0139463
990S-0139750
990S-0139763
990S-0139817
990S-0139819
990S-0140353
                                                                                                                                                                                     2000EP-0301439
                                                            Arabidopsis thaliana
                                                                                                                                                                                                                      25 - FEB - 1999; 05 - MAR - 1999; 23 - MAR - 1999; 23 - MAR - 1999; 25 - MAR - 1999; 23 - APR - 1999; 23 - APR - 1999; 23 - APR - 1999; 24 - APR - 1999; 25 - APR - 1999; 26 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - APR - 1999; 29 - MAY - 1999; 20 - M
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20 - MAY - 1999

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28 - MAY - 1999

30 - JUN - 1999

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33 - JUN - 1999

32 - JUN - 1999

33 - JUN - 1999

34 - JUN - 1999

35 - JUN - 1999

37 - JUN - 1999
                                                                                                                                                                                 25-FEB-2000;
                                                                                                    EP1033405-A2
                                                                                                                                         06-SEP-2000
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9905 - 0140823 9905 - 0140823 9905 - 01410842 9905 - 01412842 9905 - 0142390 9905 - 0142390 9905 - 0142390 9905 - 0142924 9905 - 0142924 9905 - 0142924 9905 - 0144362 9905 - 0144362 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0144335 9905 - 0145918 9905 - 0145918 9905 - 0145918 9905 - 0147303 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723 9905 - 0149723

-JUL-1

03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999;

-AUG-1999

09-AUG-1999 10-AUG-1999 11-AUG-1999 12-AUG-1999 13-AUG-1999 14-AUG-1999 16-AUG-1999 16-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 25-AUG-1999

31-AUG-1999 01-SEP-1999 σ

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferae activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                         which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic acyl transferase; transformation; anthocyanin pigment;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.2; DB 17; Length 1479;
Pred. No. 77;
2; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plants; acylation; colour; tone; colouration; colour change; Gentiana triflora; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.

    for transforming

                                                                                                                                                                      Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1479 BP; 420 A; 316 C; 331 G; 411 T; 1 other;
3..1343
/*tag= a
/product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product- Aromatic acyl transferase.
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                                                                                                                                                                                                                                   coding for aromatic acyl transferase
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                                                                                                                                                                                                                                                                           Claim 4; Page 65-69; 94pp: Japanese.
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                                                                                                                                                                               Tanaka Y, Yonekura K;
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                                                                                                      95JP-0046534.
95JP-0067159.
95JP-0196915.
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Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                    16-FEB-1996;
                                           WO9625500-A1
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                                                              22-AUG-1996.
                                                                                                       30-JAN-1996;
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                                                                                                                   17-FEB-1995
                                                                                                                                                                                Nakao M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perilla ocimoides (Clone pSAT208).
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         990S-0153070.
990S-0153758.
990S-0154018.
990S-0154039.
990S-0155139.
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99US-0161359.
99US-0161360.
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76.58;
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                                                                                                                                                                                                                                                     99US-0159638.
                                                                                                                                                                                                                                                                            99us-0160741.
                                                                                                                                                                                                              99US-0159329
                                                                                                                                                                                                                                              99US-0159637
                                                                                                                                                                                                                                                                                      99US-0160767
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                                                                                                                                                                                                                                                                                                           99US-0160770
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99US-0160980
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|1186 gatttcggttggggtaa 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                 99US-015
99US-015
                                                                                                                 99US-01
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Best Local Similarity
                                                                                24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT37311;
                                                                                                                                                                                                                                                     14-OCT-19
18-OCT-19
                                                                                                                                                                                                                                            14-OCT-1
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plants

plants

plant origin

us-08-894-356c-22.rng

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with aromatic act transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT3108-173131. NOTE: This sequence is supposed to cross reference with the protein described in AAW04727, however there are so many discrepancies between the polypeptide decoded from this sequence and the polypeptide given in the specification and described in AAW04727 that the indexer decided not to cross reference the two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA related with fruit ripening - can be used to genetically modify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "contains a putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canteloupe charentais; fruit ripening control; promoter; ss.
                                                                                                                   which produce anthocyanin pigments and thus altering colour e.g. of flowers
                                    Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1518 BP; 384 A; 340 C; 366 G; 428 T; 0 other;
                                                                                                                                                                                                                            Vectors containing DNA fragments encoding proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Karvouni 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14.2; I
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melon ripening-related cDNA clone MEL2.
                                  Fukul Y,
                                                                                                                                                                                           Claim 4; Page 73-76; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1385..1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              John I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT89415 standard; cDNA; 1526 BP.
                                                   Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.58;
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1176 gattttggatggggtaa 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 76.5
Matches 13; Conservative
                                  Fujiwara H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Greierson D,
(SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-503108/46.
                                                                                    WPI; 1996-393401/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melon cultivar
ethylene; MEL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumis melo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09737023-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-1997;
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                                  Ashikari T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aggelis A,
                                                     Nakao M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                      DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic acyl transferase; transformation; anthocyanin pigment; plants; acylation; colour; tone; colouration; colour change; Gentiana trifloza; Petunia hybrida; Perilla ocimoides; Scenecio cruentus; Lavandula angustifolia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 17; Length 1508; Pred. No. 77;
                                                                                                                                                          Kusumi T, Mizutani M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1508 BP; 442 A; 294 C; 295 G; 477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Aromatic acyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic acyl transferase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT37313 standard; cDNA to mRNA; 1518 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lavandula angustifolia (Clone pLAT21)
                                                                                                                                                      Ashikari T, Fujiwara H, Fukui Y,
Nakao M, Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                                                               Claim 4; Page 69-72; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%;
76.5%;
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95JP-0067159.
95JP-0196915.
                96WO-JP00348
                                                                  95JP-0067159.
                                                 96JP-0046534
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|1182 gattttgggtgggggaa 1198
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Matches 13; Conservative
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                                                                                                                                                                                                          WPI; 1996-393401/39.
P-PSDB; AAW04726.
                                                                                                                       SUNR ) SUNTORY LTD
              16-FEB-1996;
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                                                 30-JAN-1996;
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29-JUN-1995;
                                                                17-FEB-1995;
                                                                                    29-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT37313;
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Length 1518;

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                                                                    novel ripening-related product from Cucumis melo. It is one of two specified sequences (MEL2) 1526 bp or (MEL7) 686 bp which were 1solated from a melon ripe fruit cDNA library. MEL2 is not a full-length clone; it lacks the initiation codon for the amino terminus. The cDNA allows control of the ripening of fruit, especially melons.
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anther specific cDNA or genomic sequences can be used to identify and isolate anther specific promoters. The anther specific promoter can then be cloned into a recombinant construct and used to express heterologous genes. Preferred heterologous genes include Diptheria toxin A-chain gene; pectate lyase gene pelE from Erwinia chrysanthemi; T-urfil from cms-T maize mitochondrial genomes; the Gin recombinase gene from phage Mu; the indole acetic acid-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plants; male sterility; pollen; sterile; seel febilination; seed; hybrid; toxin-A; pelE; T-urfil3; Gin; iaal; CytA; toxin; Nicotiana tabacum; Diptheria; Erwinia chrysanthemi; phage Mu; Psuedomonas syringae; Bacillus thuringiensis; anther;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anther-specific cDNA, genomic and recombinant DNA - produce transgenic male-sterile plants, which prevents self-pollination,
                                                                                                                                                                                                                               ;
                                                                                                                                                                                                   Length 1526;
                                                                                                                                                         Sequence 1526 BP; 439 A; 297 C; 331 G; 448 T; 2 U; 9 other;
                                                     cDNA sequence is from the MEL2 clone which produces a
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                   83.5%; Score 14.2; DB 18; 76.5%; Pred. No. 77;
                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                               2; Mismatches
 especially melons to control ripening
                            Claim 1; Pages 18-19; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
66..1412
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anther specific cDNA clone ant32.
                                                                                                                                                                                                                                                                                                                                                            AAQ54685 standard; cDNA; 1542 BP
                                                                                                                                                                                                                                                                                    1136 gactttggatggggaaa 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93EP-0810455
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                          1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuttle AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in hybrid seed prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-010428/02.
P-PSDB; AAR47475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crossland LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP578611-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breeding;
                                                                                                                                                                                                                                                                                                                                                                                       AAQ54685;
                                                                                                                                                                                                   Query Match
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                                                       This
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CC from Bacillus thuringiensis Israeliensis. All of these genes when CC expressed in anther tissue will result in the inability of the CD plant to produce viable pollen. Transformation of plants with such CC a recombinant construct can produce transgenic, male sterile plants. CC Male sterility is important in the production of hybrid seeds as it CC prevents self pollination which hinders breeding and hybrid seed CC production.
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Sequence 1542 BP; 473 A: 293 C; 332 G; 444 T; 0 other;

Overy Match 83.5%; Score 14.2; DB 15; Length 1542; Best Local Similarity 76.5%; Pred. No. 77; Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps

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Qy 1 GAYTTYGGNTGGGGNAA 1.7

Search completed: November 5, 2001, 18:12:09 Job time: 15464 sec

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US-07-598-873-1
Query Match
Best Local Si
Matches 13;
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                                                                                                   ; Search time 168.74 Seconds (without alignments) 19.072 Million cell updates/sec
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Sequence 1, Ap
Sequence 1, Ap
Sequence 5, Ap
Sequence 74, A
Sequence 24, A
Sequence 24, A
Sequence 24, A
Sequence 24, A
Sequence 1, Ap
Sequence 1, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6,
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Sequence 1,
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Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Sequence Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-07-695-472B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-695-472B-34
US-07-695-472B-36
US-07-916-098A-44
                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                       324599 seqs, 94655562 residues
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                                                                                                     November 5, 2001, 18:05:10
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Listing first 45 summaries
                                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                             1 GAYTTYGGNTGGGGNAA 17
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                                                                                                                                                        US-08-894-356C-22
                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                               Perfect score:
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                                                                                                                                                                                             Seguence:
                                                                                                                                                                                                                                                                       Searched:
                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                 Title:
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US-09-187-050-6/C

Sequence 6, Application US/U9187050B

Sequence 6, Application US/U9187050B

Sequence 6, Application US/U9187050B

PAPLICANT: Croteau, Rodney B

APPLICANT: Croteau, Rodney B

TITLE OF INVEWTION: Nucleic Acids Encoding Taxus Geranylgeranyl Diphosphate

TITLE OF INVEWTION: Synthase, And Methods of Use

TITLE NET REPRESENCE: WSUB1243

FILE REPERENCE: WSUB1243

CURRENT APPLICATION NUMBER: US/09/187,050B

CURRENT APPLICATION NUMBER: US/09/187,050B

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

EMOTTH: 23
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                                  Sequence 1, Appli
Sequence 4, Appli
Sequence 35, Appli
Sequence 59, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 150, Appli
                                                                                                                                                                                                                                                                                   Sequence 4, Appli
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: non-degenerate OTHER INFORMATION: reverse PCR primer
                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS TITLE OF INVENTION: DERIVED THEREFROM NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_difference
LOCATION: (1)..(23)
CTHER INFERMATION: No. 6043072-degenerate PCR primer
US-09-187-050-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.5%; Score 14.2; DB 3; 76.5%; Pred. No. 8.4; 11ve 2; Mismatches 2;
              US-08-295-502-1

US-08-295-502-1

US-08-519-547A-5

US-07-695-472B-4

US-07-49-446-1

US-07-749-446-1

US-07-749-646-1

US-07-749-646-1

US-08-149-101A-5

PCT-US94-1283-5

US-08-906-616-150

US-08-906-616-150

US-08-906-614-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-150

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-09-012-692-160

US-08-906-613-150

US-08-906-613-150
                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/07598873; Patent No. 5254800; GENERAL INFORMATION; APPLICANT: BIRD, COLIN R; APPLICANT: GRIERSON, DONALD; APPLICANT: RAY, JOHN A; APPLICANT: SCHUCH, WOLFGANG W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAYTTYGGNTGGGGNAA 17
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GATTTCGCCTGGGGTAA 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: GRIERSON, DONALD
APPLICANT: GRIERSON, DONALD
APPLICANT: SCHUCH, WOLFGANG W
TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: Ninth Floor, 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,531
                                                                                                                                                                                                                                                                                                                              ORGANISM: Lycopersicon esculentum
STRAIN: Ailsa Craig
DEVELOPMENTAL STAGE: Ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,037
FILING DATE: 16-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08396531 Patent No. 5744364
                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-861-3004
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-661-3000
TELERAX: 202-822-0944
TELERAX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:||:|| ||||| ||
866 GATTTTGGATGGGGAAA 882
                       NAME: DEAVER, DONALD B REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          US-08-073-425-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-396-531-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/598,873
FILING DATE: 19901019
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEFAS: 202-822-0944
INFORMATION FOR EQ ID NO: 1:
SECURENCE CARRACTERISTICS:
LENGTH: 1080 base pairs
TYPE: NUCLEIC ACID
STRANDEDESS: double
TOPOLOGY: linear
3: CUSHMAN, DARBY & CUSHMAN
Eleventh Floor, 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.2; DE Pred. No. 14; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BONINELL, JEREMY M.
APPLICANT: BONINELL, JEREMY M.
APPLICANT: GRIERSON, DONALD
APPLICANT: RAY, JOHN A
APPLICANT: ROUCH, WOLFGANG W
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARRY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/08073425
; Patent No. 5569829
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Ailsa Craig
DEVELOPMENTAL STAGE: Ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 76.5
Matches 13; Conservative
                                       Washington
                                                                                 COUNTRY: USA
ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-073-425-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-598-873-1
                                                              STATE:
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Gaps

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APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
                                                                      ö
                                    Length 1512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1542;
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-106S/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
                                      DB 3;
                                    Score 14.2; DE
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%; Score 14.2; I
76.5%; Pred. No. 15;
iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Lazar, Steven R. REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          CIBA-GEIGY Corporation
                                                                                                                                                                                                 RESULT 7
US-08-207-904-1
; Sequence 1, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (919)541-8615
(919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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| 1239 GATTTTGGGTGGGGAAA 1255
                                                                                                                                7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAYTTYGGNTGGGGNAA 17
                                                                                                           1 GAYTTYGGNTGGGGNAA 17
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Nicotiana
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66..1412
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 7 SKyller
CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                      Query Match
Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-207-904-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                     Score 14.2; DB 1; Length 1080;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1096;
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Atkinson, Richard L.
APPLICANT: Atkinson, Richard L.
APPLICANT: Dhurandhar, Nikhil V.
TITLE OF INVENTION: Viral Obesity Methods and Compositions
FILE REFERENCE: 710395.90010
CURRENT APPLICATION NUMBER: US/09/056,153
CURRENT FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                         Indels
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Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCORDINGS

APPLICANT: Aggelis, Alexandros
APPLICANT: Gererson, Donald
APPLICANT: Gererson, Donald
APPLICANT: Gererson, Donald
TILE OF INVENTION: Fruit Ripening
TILE REFERENCE: SEE50111/UST
CURRENT APPLICATION NUMBER: US/09/142,514A
CURRENT FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: GB 9606906.7
EARLIER FILING DATE: 1997-03-24
EARLIER FILING DATE: 1996-04-02
SAPTWARE: PALENTION NOWER: GB 9606906.7
EARLIER FILING DATE: 1996-04-02
SOFTWARE: PALENTIN VOY: 2.0
                                                                                                                                                                                                                                         2; Mismatches
                                                                        , OKGANISM: Lycopersicon esculentum; STRAIN: Ailsa Craig; DEVELOPMENTAL STAGE: Ripening US-08-396-531-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09142514A Patent No. 6107548
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/09056153; Patent No. 6127113
               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                     83.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Adenovirus type 36P
US-09-056-153-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                 Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                         1 GAYTTYGGNTGGGGNAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.5
Best Local Similarity 76.5
Matches 13; Conservative
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Cucumis melo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1512
                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-056-153-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-142-514-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Gaps

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APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: Murphy, T.J.
APPLICANT: Mishida, Ken'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,245
FILING DATE: 19920702
                                           Sequence 1, Application US/07908245 Patent No. 5498539
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.
ZIP: 30309-4530
                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
                         JS-07-908-245-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-908-245-1
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                                                                                                   APPLICANT: Tuttle, AnnMarie
APPLICANT: Tuttle, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 2.1
CORRESPONDENCE ADDRESS:
ADDRESSE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: New York
COUNTRY: USA
ZIP: 10532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: /note= "Putative transcription CTHER INFORMATION: start site"
US-08-207-904-16
                                                                                                                                                                                                                                                                                                                                                        ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.2; DE
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Nicotiana tabacum
INDIVIDUAL ISOLATE: Ant32 genomic clone
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTARTION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC 1624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8615
TELEGAX: (919)541-8615
RESULT 8
US-08-207-904-16
Sequence 16, Application US/08207904
Patent No. 5477002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.5%;
ilarity 76.5%;
Conservative
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2076..3422
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Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
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Sequence 5, Application US/09123708

Sequence 5, Application US/09123708

Sequence 5, Application US/09123708

GENERAL INFORMATION:

APPLICANT: SCHRADER, Juergen

APPLICANT: OSDBOCKE, Axel

TITLE OF INVENTION: TREATHENT OF VASCULAR DISORDERS

FILE REFERENCE: 511169-2003

CURRENT APPLICATION UNMER: US/09/123,708

CURRENT FILING DATE: 1998-07-28

EARLIER APPLICATION NUMBER: 08/553,503
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85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13;
Pred. No.
FILING DATE: 19920702
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFRENCE/POCKET UNMER: EMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                    TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4089 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3840 GACTTAGGGTGGGGAAA 3824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Bovine
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3249 GATTTGGGTGGGGAAA 3265

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Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-822-028-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-479-285-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SCHRADER, Jurgen
APPLICANT: SCHRADER, Jurgen
APPLICANT: GOBECKE, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 511169-2004
CURRENT FILING DATE: 1998-07-28
CURRENT APPLICATION NUMBER: 08/05/123,624
CURRENT APPLICATION NUMBER: 08/553,503
PRIOR FILING DATE: 1996-03-01
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 5
LENGTH: 4097
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MEZES, PETER S
APPLICANT: MEZES, PETER S
APPLICANT: MEXEN
APPLICANT: RIXON, MARK W
APPLICANT: RAPLAN, DONALD A
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLOW, JEFFREY
TITLE OF INVENTION: MOUFLED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
STREET: P.O. BOX 1967
CITY: MIDLAND
                                                                                                                                                                                                                                                                        ö
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Pred. No. 85;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13; DB
Pred. No. 85;
                EARLIER APPLICATION NUMBER: P4411402.8
EARLIER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 74, Application US/08822028
Patent No. 5993813
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09123624 Patent No. 6149936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.58;
EARLIER FILING DATE: 1996-03-01
                                                                                                                                                                                                                                 76.5%;
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3868 GACTTAGGGTGGGGAAA 3852
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                                                                                                                                                                                                                                                                                                            1 GAYTTYGGNTGGGGNAA 17
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                                                                                                                                                                                                                               Ouery Match 76.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.5
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                 TYPE: DNA
CYCOMEGALISM: Cytomegalovirus
US-09-123-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bos taurus
US-09-123-624-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-123-624-5/c
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Sequence 74, Application US/08479285

Patent No. 6207815

GENERAL INFORMATION:
APPLICANT: GOURLIE, BRIAN B
APPLICANT: RIXON, MARK W
APPLICANT: RIXON, WARK W
TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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COUNTRY: USA

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PATENT PC-DOS/MS-DOS

SOFTWARE: PATENT Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/08/479,285

PTING DATE: 07-JUN-1995

TING DATE: 07-JUN-1995

TOTALER

TO
                                                                                                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12.6; DB 2;
Pred. No. 1.1e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-8104
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,028
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-19/3
ATTORNEY/AGENT INPORMATION:
ZIP: 48641-1967
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.18;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAYTTYGGNTGGGGNAA 17
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P.O. BOX 1967
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1 GAYTTYGGNTGGGGNAA 17
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                                                                                                    RESULT 15
US-08-646-590B-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WARREN, PATLICK V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 32
CORRESPONDENCES: 32
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
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ZUP: 17068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCULENTLY
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636 8104
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 24, Application US/08599171A; Patent No. 5814473
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: HERNON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 3314(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAN: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: LINEAR MOLECULE TYPE: GENOMIC DNA
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                                                                                                                                     LENGTH: 508 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STRANDEDNESS: SINGLE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Matches 12; Conserve
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US-08-599-171A-24
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US-08-479-285-74
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STATE: NE
COUNTRY:
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Sequence 24, Application US/08646590B

Patent No. 596228

GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Swanson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.1%; Score 12.6; DB 2;
70.6%; Pred. No. 1.2e+02;
Live 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
COMPUTER: DISKETTE
COMPUTER: DISKET WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,590B
FILING DATE: US/08/646,590B
FILING DATE: US/08/646,590B
FILING DATE: US/08/646,590B
FILING DATE: 08-MAN-1996
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 21-January-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REFERENTALON NUMBER: 38,347
REFERENTION NUMBER: 38,347
REFERENTALON NUMBER: 38,347
                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson, P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CA
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TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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; LOCATION: 1...909
US-08-646-590B-24
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 12; Conservative
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74.1%; Score 12.6; DB 1; Length 912; 70.6%; Pred. No. 1.2e+02; Live 2; Mismatches 3; Indels

Conservative

Query Match Best Local Similarity Matches 12; Conserva

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27.627 Million cell updates/sec
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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gb_est110:* gb_htc:* em_gss_fun:* em_gss_hum1:* em_gss_hum3:* em_gss_hum3:* em_gss_hum3:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum7:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:* em_gss_hum9:*	ស្តេស្តេស្តេស្តេស្តេស្តេស្តេស្តេស្តេស្តេ	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,K., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           info@genomesystems.com web site: www.genomesystems.com
Insert Length: 489 Std Error: 0.00
Seq primer: -40RF from Gibco
High quality sequence stop: 212
POLYA=No.
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/lab_host="XL10-Gold"
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BB264508 BB264508
AWA71629 s13101.y
A2813888 2M0081B21.y
A281388 ZM0081B21.y
A0034368 CIT-HSP-2
BE460581 EST412000
BL378020 MLBB35D12
BG508347 sac95e04.
AW350546 GM210009A
RG365 y110f04.s1
A1967062 496021B11
AU096989 AU096989
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BE213479 GF-FV-P6E
BG042849 saa45f04.
BE020415 sm43h12.y
AV539490 AV539490
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AQ186186 HS_3074_B
BF009723 S834002.y
BG442050 GA_E8001
BG444080 GA_E8002
AA713159 32719 Lam
BE332935 SET399380
AI899217 EST268660
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AW650512 EST328966
BF324543 su25c03.y
AI856260 sb39912.x
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BF840553 RC6-HT100
AW318655 un03b01.y
BE461054 EST412473
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AZ015624 RPCI-23-2
AA650754 30868 Lam
BG046171 saa49e12.
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AI748527 sb54c08.y
AV425743 AV425743
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Glycine.
1 (bases 1 to 227)
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
                                                                                                                                                                                            AI494813 sa96g04.y
AW234169 sf22a08.y
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                                    SUMMARIES
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BF009723
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AUTHORS
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Gaps

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Score 14.2; DB 113; Lower Pred. No. 1.2e+03; Indels
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1. .247
Cultivar="TyCopersicon esculentum" /cultivar="TAA96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="tomato ovary, TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University Genomics Institute
Clemson University
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/clone="cLED21D13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: dfrisch@CLEMSON.EDU.
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                                                                                                                                                                                                                                                                                          AI488429.1 GI:4383800
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                                             83.5%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: David Frisch
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                                                                                Matches 13; Conservative
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                                             Query Match
Best Local Similarity
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Best Local Similarity
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida; Erabales; Fabaceae; Papilionoldeae; Glycine.

(Dasss 1 to 244)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Bowers,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
             AW234169 244 bp mRNA EST 17-JUL-2000 sf22a08.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-687 5' similar to TR:Q43583 Q43583 HSR201 PROTEIN: ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomessystems.com or info@genomessystems.com web site: www.genomessystems.com Insert Length: 486 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1028-687"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="roots of 'Supernod' plants" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilbrary was constructed by Dr. Coryell." 37 c 65 q 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_l1b="Gm-c1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                           AW234169.1 GI:6566526
                                                                                                                                            Glycine max
Eukaryota; V
                                                                                                                              soybean.
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                            DEFINITION
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AW234169
                                                                                                            KEYWORDS
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Alcala, J. Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notew_Nector: pBlueScript SK(-); Site_1: EcoR1; Site_2: ANO1: cLED - Tomato Carpel EST Library OligodT-primed and directionally cloned cDNA in vector Lamda 2AP II with 5' and 3' ends located at the EcoR1 and ANO1 sites,
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947076G02.x2 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF"
                                                                                                                                                                                                                                                                                                                                    EST 247 bp mRNA EST 29-JUN-1999 EST2146768 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cEED21913, mRNA sequence.
                                                                    Gaps
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 258)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,E., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Crgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially disested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

3 C 6 69 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                       Dmail: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resqon.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
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Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg.,E.
Lansing,Ml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 249;
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Pred. No. 1.2e+03;
2; Mismatches 2; I.
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                                                                                                                                                                                                                                                                             1. .249
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      /db_xxref="taxon:10090"
/clone='RPCI-23-258D7"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 517-353-9168
Email: 22313tcn@lbm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7 dye primer.
Location/Qualifiers
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AA650754.1 GI:2580846
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76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Megann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-22-258D7.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Fig. 101 838 0200
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                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 247)
Walbot, V.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 249)
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RPCI-23-258D7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-258D7,
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                                                                                                                                                                                                                            Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: walbotestanford.edu
Plate: 94/706 row: G column: 02.
Location/qualifiers
1. 247
/organism="zea mays"
/cultivar="B73"
/db_res="taxon:4577"
/clone_lib="947 - 2 week shoot from Barkan lab"
/tissue_tstage="zea and stem, including leaf base"
/dev_stage="zea week old seedling (3 leaves)"
/lab_host="XL1-Blue"
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                                                                                                                                                                                                                                               University
Unpublished (1999)
Contact: Walbot V
Contact: Walbot V
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Fax: 650 725 8221
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BG550470.1 GI:13562250
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Mus musculus
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Zea mays
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1 (Dasss 1 to 259)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Bowers,R., Waterston,R. and Wilson,R.

Public Soybean EST Project
Unpublished (1999)
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430.0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 157.

Location/Qualifiers
                                                                                                /note=-Vector: lambda Z1p-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA
                                                                                                                                                                                                                                                                                                                  inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG046171 259 bp mRNA EST 25-JAN-2001 saa49e12.y1 Gm-c1060 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1060-215 5' similar to TR:Q43583 Q43583 HSR201 PROTEIN. ;,
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Publit Soybean EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone_lib="Gm-c1060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 258;
                                                                                                                                                                                                                                                                                                                                                                         10 others
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14.2; DB 10;
Pred. No. 1.2e+03;
2; Mismatches 2;
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                                                                             /clone_lib="Lambda-PRL2"
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/strain-"var columbia"
                              /db_xref="taxon:3702"
                                                    /clone="281H6T7"
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BG046171.1 GI:12494655
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76.5%;
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Fax: 314 286 1810
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/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_rraf="taxon:3702"
/clone="168A5xp"
/clone="168A5
from root tissue of 2 week old seedlings for PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI. XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases I to 263)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis CDNA clones
Plant Physiol. 106, 1241-1255 (1994)
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31149 Lambda-PRL2 Arabidopsis thaliana cDNA clone 168A5XP 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
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MSU-DOE Plant Research Laboratory
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Fat: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
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Location/Qualifiers
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AUTHORS
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10 others

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ORIGIN

DEFINITION RESULT 9 A1608251/c

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ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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Email: genome-resettc.riken.go.jp,
URL:http://genome-resettc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp/
Carninci,P., Nishliyama,Y., Westowcer,A., Itoh,M., Nagaoka,S., Sasaki,
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                       Konno, H., Atzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horz, F., Ishii, Y., Ishikawa, T., Itoh, M., Itacawa, M., Kadota, K., Kayawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Niki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, Y., Tan, K., Yano, K., Yano, M., Watahiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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transcriptase and subsequently enriched for full-length by
cap-trapper. Obly went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
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                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
/clone="A330015g22"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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The Institute of Physical and Chemical Research (RIKEN), Genomic
                            BB264508 294 bp mRNA EST 07-JUL-2000 BB264508 RIKEN full-length enriched, 10 days neonate cortex Mus musculus CDNA clone A830015622 3', mRNA sequence.
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/dev_stagh="10 days neonate"
/lab_host-"DH10B"
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                           (bases 1 to 294)
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Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter F., Kann, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. primer: SalI(dT): 5'-CGGTCGACCGTCGACGGTTTTTTTTTTTTT3'. CDNAs were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                              pp mRNA EST 21-APR-1999
Solter mouse embryonic stem cell Mus musculus
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/db_xref="taxon:10090"
/clone="IMAGE:894569"
/clone="IMAGE:894569"
/dev_stage="embryo"
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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CDNA clone IMAGE:894569 3', mRNA sequence.
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Pred. No. 1.2e+03;
2; Mismatches 2;
                                                                                      Score 14.2; DB 10;
Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
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76.5%;
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Best Local Similarity 76.5
Matches 13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
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TITLE JOURNAL COMMENT

FEATURES

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CDNA library was constructed from mRNA isolated from very vong cotyledons (20-50mgs fresh weight) of greenhouse groun plants. The library was prepared using the Life Technologies propersoript convaint in the Life Complementary DNA was synthesized from mRNA using a poly(df) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosladae; eurosida; Fabales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 307)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Sohurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
Call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 301.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                           Length 294;
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Pred. No. 1.2e+03;
Hismatches 2; Indels
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Public Soybean EST Project
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AW471629.1 GI:7041735
                                                                                                                                                                                                                                                        83.5%;
76.5%;
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Fax: 314 286 1810
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Holians, Fabales; Fabaceae; Papilionoideae; Glycine.

El (bases 1 to 324)

El (bases 1 to 324)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bohla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Pape,D., Harvey,N., Schurk,R., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Matterston,R. and Wilson,R.

AL Waterston,R. and Wilson,R.

AL Upublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Mashington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108, USA

Tel: 314 286 1800

Fax: 40000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIB56623 324 bp mRNA EST 16-JUL-1999 sb39g12.yl Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1014-95 5' similar to TR:004201 004201 HYPERSENSITIVITY-RELATED GENE 201 ISOLOG.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote—"Vector: pT7T3Pac (pT7T3, Pharmacia); Site_1: ECORI; Site_2: HindIII; This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. ECORI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with ECORI and HindIII. The cDNA fragments were directionally cloned into the ECORI-HindIII restriction site of the pT7T3-Pac vector. The ligated cDNA fragments
                                                                                                                                                                                                                                                                                                                                                                  ö
site of the pSPORII vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
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                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                       Score 14.2; DB 116; Length 307;
Pred. No. 1.2e+03;
Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                       83.5%;
ilarity 76.5%;
Conservative
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nes 13; Conserv
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Mammalis Butneria; Pirmates; Catarinin; Hominidae; Homo.

R dams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end Search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13-21

Class: BAC ends.
    purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ034368 333 bp DNA GSS 11-JUL-1998
CIT-HSP-2319K4.TF CIT-HSP Homo sapiens genomic clone 2319K4, DNA
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                            Score 14.2; DB 250; Length 331;
Pred. No. 1.2e+03;
2; Mismatches 2; Indels 0;
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Pred. No. 1.2e+03;
2; Mismatches 2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="231944"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT-HSP"
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AQ034368
AQ034368.1 GI:3300542
GSS.
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76.5%;
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76.5%;
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                                                                                                                                                                                                                                                                                                                   115 GATTTTGGCTGGGGAAA 131
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Best Local Similarity 76.5
Matches 13; Conservative
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BE460581/c
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AQ034368/C
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                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 31)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., 181am, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Welss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mosee, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding." 49 c 101 g 79 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                      AZB13888 331 bp DNA GSS ZU-FEB-ZUUL
ZM0081B21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male" | //sex="Male" | //sex="Male" | //sex="Male" | //sex="Male" | //sex="E. Coli strain XLIO-Gold, T1-resistant, F-" | //note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                  Score 14.2; DB 102; Length 324; Pred. No. 1.2e+03; 2; Mismatches 2; Indels 0;
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC2MO081B21"
/clone=!UGC2MO081B21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: B column: 21
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone UUGC2M0081B21 F, DNA sequence.
AZ813888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 331.
Location/Qualiflers
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                                                                                                                                                                    83.5%;
76.5%;
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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Best Local Similarity
Matches 13; Conserv
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A2813888
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COMMENT

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/note="Vector: pBluescriptSKmcUadapt; Site_1: EcoR1; Site_2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp." 71 c 40 g 116 tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                  Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                      1 (bases 1 to 347)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley
3E460581 347 bp mRNA EST 27-JUL-2000 EST412000 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA clone cLEG31N6, mRNA sequence.
BE460581. GI:9504883
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Generation of ESTs from tomato fruit tissue, breaker stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 347
/organism="Lycopersicon esculentum"
/organism="TA496"
/db_xref="taxon:4081"
/clone="cLEG31N6"
/clone_lib="tomato breaker fruit, TIGR"
/tissue_type="Pericarp"
/dev_stage="breaker"
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Contact: David Frisch
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Clemson University
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Email: dfrisch@CLEMSON.EDU
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